

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC  
 TGCAGACTAAACCAGTCATTACTTGTGTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
 TGGATCACTGGCGTTATCCTTCTTGCA GTTGGCATTG GGGCAAGGTGAGCCTGGAGAATTA  
 CTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
 TCATTATTCTTTTGGGCACCTTTGGTTGTTTGGCTACCTGCCGAGCTTCTGCATGGATGCTA  
 AAAGTGTATGCAATGTTTCTGACTCTCGTTT TTTGGT CGAAGTGGTGCCTGCCATCGTAGG  
 ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
 TGGTTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
 TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAAGTAAACA  
 ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
 ATTTCTTTTGGAGTTGCTTGCTTCCAAGTATGGAATCTTTCTCGCCTACTGCCWCTCTCG  
 TGCCATAACAAATAACCAAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCTCTCT  
 CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
 ACAACACTACTTACTGATAGACAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
 GTAGACCTAAAACCTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTTCATGTTAGATCG  
 TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

**FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902  
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown  
><MW: -1, pI: 8.36, NX(S/T): 1  
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLENYFSLLEKATNVPF  
VLIATGTVIIILGTGFCFATCRASAWMLKLYAMFLTIVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCGACCGCGTCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
 GCCGGGGTAGGCTCTGGAAGGGGCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAAGAGGGT  
 GTTCCCTCTTTTCGGGGTCTCACCAGAAGAGGTTCTTGGGGTTCGCCCTCTGAGGAGGGT  
 GCGGCTAACAGGGCCGAAACTGCCATTGGATGTCCAGAATCCCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTC  
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAGTAACTGAAACTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCTAGGGACTGGAGGTGCCGCTACTACCATGGTAATCCTGTATCTG  
 CCGAGATGACAGTGGAAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACACGGGACCTGTTTCGGCCACCAAGGAGGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT  
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGAAT  
 GAAAAGTGTTCGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGCTTGAAATGTCTAAATGTTTC  
 TGTAGCAGAAAACAGATAAAGCTATGATCTTTATTAGAG

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# FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPFRGRGPHEPRRKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTACAGCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACAGGGTCCCCTACCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

1002065.2222

MEEGNGLGLIKMVHLLVLSGAWGMQMWVTFVSGFLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLTATVNARWLEPRTTAAMWALQTVEKER  
GLGGVEVPGSHOGPDPIYROLREKDPKYSALRONFFRYHGLSSLNLCGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

AATTCAAGATTTTAAGCCCATTTCTGCAGTGGAAATTTTCATGAAGTACGACAGAGGACACCATCTT  
CTTGATTATACAGAAGAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
AGAAGCTTTTGATAAAAAGGGATTTCATGTAATCGCTGCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAGTTGGGGAGAAAGGTCTCTGGGT  
CTGATCAATAATGCTGGTGTCCCGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATAGTGTGACACTAAATATGCTTC  
CTTTGCTCAAGAAAGCTCAAGGAGAGATTATTAATGCTCCAGTGTTGGAGTGCCTTGCA  
ATTCGTTGGAGGGGCTATACCTCCAAATGACGTGGAAGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCAATGAACAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAACCTGCCATTGGGAGCAGCTGTCTCCA  
GACATCAAAACAACATATGGAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTCTGGATACCTCTG  
TCTCATATGCCAGCAGCTTTCGAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAGAACACATCTCCTTTTCAACCCCATTCCTATCTGTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCACCATCGTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCATATAGGCAAGTCTGCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAATTTGAAAGACTTGCCCATTCAAAATG  
AATCTTACCCTGGCCTGCCCAATGCTTATGGTCCCCAGCATTTCAGTAACCTTGTGAATGTT  
AGCTACATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

### FIGURE 8

Important features of the protein:

amino acids 1-17

## amino acids 136-152

## amino acids 161-163, 187-190 and 253-256

## amino acids 39-42

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCCT  
 GTAGTCATGTACCCACCGCCGCGCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGCGCTCGTGCTGGAGGAATGGA  
 AGCAACTGTCGAGATTGACGCGGAATATGATTCTCTTCCTCCTTGCTTTTCTGCTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTTGAAAGCTCTGGCTTTGAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAACACGCAAAATCCACCCTCTTACCAG  
 CTCTCAGAAAGCGGACACCGACCTTGAGAACTTACCTGAGATTTCGTCACAGAAGACACA  
 AGACACATCCAGCGGGGACCACTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAGCCCCCTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCAG  
 CTCCCTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCACTCTGAACATATCGCCAGAAAGGCGTGATTGACGCTTCTCCTGCATGCATGGA  
 AAGGATACCGCAAGTTTTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTTGGATCTTGGGTCT  
 GAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTGCAAGAAGTTACATTTGAAAAGGAGC  
 TGGACGTCAACCTGTTTGAAGACACGATCCGCACTCGCATCTGGGGGGGCTCCTGAGTGCTTACCAC  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCTCGTC  
 CTTCAGAACACCAATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGATTTGCCAAC  
 CGCCACGGTGACCTCCGACAGCACTGTGGCCGAGGTACCAAGCATTGAGCTGGAGTTCCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCTGTCTGGGAAGAAGGATGGGCTGGTGCCATGTTCATCAATACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAACCGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACCGCCGCTTCAGTGCCAAGATGGACACCTGGTGCTTCTTGCCA  
 GGGACGCTGGCTCGGGCGTCTACCAAGGCTGCCCCGCCAGCCACATGGAGCTGGCCAGGA  
 GCTCATGGAGACTTGTATACAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGACGCTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTTCACTGTACCGGCTCACAGGGGA  
 CCGCAATACCAAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC  
 CCTCGGCTGGCTATTCTTCCATCAACATGTCCAGGATCCTCAGAAGCCGAGCCATAGGAG  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTTCTTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCTTACGTGTTCAACACCGAAGCCCCACCTCTGCCTATCT  
 GGACCTCGCT**TAG**GGTGGATGGCTGCTGCTGGTGTGGGGACTTCGGGTGGGACAGGCACTTG  
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGCTAGCACCGGCAACCGGCAAGTGGGCCAGGCT  
 CTGAACCTGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGCTGAGGACAACTGA  
 GGGCTCTGCTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCTCCTC  
 CAGAAGACACGAATCATGACTCAGGATGCTGGAAGCCTGAGCAGGTCTCTGTGGGCGGACCA  
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGCTCTGGAGGGGCTGCCGTGA  
 CTCACAGAGGCTGAGGCTCCAGGGCTGGCTCTGGTGTTCAAAGCTGGACTCAGGAGTCCCTC  
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGCAAGTCGCTGAGCTCAGGCGCCCT  
 CCAGTGAATGGGTCTTTTCGTTGAGATAAAAGTTGATTGCTCTAACCGCAA

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## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529  
><subunit 1 of 1, 699 aa, 1 stop  
><MW: 79553, pI: 7.83, NX(S/T): 0  
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPHHRDFISVTLSTFGESYDN  
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLFCGLLFYINLADHWKALAFRLBEEQKMRPE  
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT  
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTVPVHLNY  
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSSFSEWFGLGLTLIDALDTMWILGLRKEFEAA  
RKWVSKKLHFEKDVDVNLFFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
PYSVDNIGTGVAAHPPRWTSDSTVAEVTSIQLEFRELRLTGDKKFQEAWEKVTQHIHGLSGK  
KDGLVPMFINTHSGFLFTHLGVFTLGRADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
HLLRHSEPSKLTFFVGEALHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRNLLRPETVESLFYLYRVTGDRKYQDQWG  
WEILQSFSRFRTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
AYVFNTAHLPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

10020063.121301

**FIGURE 11**

GGGCGCCGCTAGGCCGGGAGGCCGGGCCGGCGGGCTGCGAGCGCTGCCCATGCGCCGCG  
CGCCTCTCCGCACGATGTTCCCTTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCGCGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
CTGCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCTTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT  
GCCCTTCGCGAACGCTTCGAGGAGCTCCTGGTCTTCTGTGCCCCACATGCGCCGCTTCTCTGA  
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCATTACAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCTTCTGAGGCTGGGC  
CCTTCCAGCTGGCTCCCCGGGAGCTCCACCCCTCTCAACCATACAAGACCATGTGCGCGCG  
ATCTCTGCTGCTCTCAAGCAGCATCTACCGGCTGTGCAATGGGATGTCTCAACCGCTTCTTGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCTCGGGAATCACAACTGGGTACAAGACATTTCCGCACCTGCATGACCAGCCTGCGCG  
AAGAGGGACCAGAAGCGCATCGAGCTCAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCGACCCACCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCTTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGCTCTGTCCG  
GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTACGTGCCACGGCCTGTGGG  
TAGTGGGAGGGCTGAACAGGACAACCTCTCATACCCCTACTCTGACCTCCTTACAGTGCCC  
AGGCTGTGGGTAGTGGGAGGGCTGAACAGGACCAACCTCTCATACCCCCAAAAA  
AA

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## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL<sub>5</sub>SLGFFSL<sub>10</sub>LWLQLSCSGDVARAVR  
GQGQETSGPPRACFPPEPPPEHWEEDASWGPHRLAVLV<sub>15</sub>PF<sub>20</sub>FRERFEELV<sub>25</sub>FVPHMR<sub>30</sub>RFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA  
SPELHPLYHYKTYVGGIILL<sub>10</sub>SKQHYRLCNGMSNR<sub>15</sub>FWG<sub>20</sub>GREDD<sub>25</sub>EYRR<sub>30</sub>IKGAGL<sub>35</sub>QLFRPSGI  
TTGYKTFRHLHDP<sub>10</sub>AWRKR<sub>15</sub>DQKRIAAQ<sub>20</sub>QEQ<sub>25</sub>QKVDREGGLNTV<sub>30</sub>KYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 29-49 (type II)

### **N-glycosylation site.**

amino acids 154-158

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

### **Tyrosine kinase phosphorylation site.**

amino acids 226-233

### **N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGCTTTATAATAAACAGTTAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1020063.121301

**FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:****Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

10020063.121301

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCGAGCGGACAAAG  
 GAGCATGTCCGCGCGGGGGAAGGCCGCTCCTCCGCGCCGCATAGGGCTCCGGTCCGCGCGTGG  
 GCCCGCGCCGCGCTCCTGCCCCCGCGGGCTCCGGGCGGCGCCGTAGGCCATGTGCGCGCGCG  
 CTCGCCCCGAGGCCCGCGGCCGCGCAGC**ATG**GAGCCACCCGACGCCGCGCGGGCGCGCGCA  
 GCCCGCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG  
 CGCGCGCGCGCGCGCGCGCTGCCCCGCGCTGCAAGCAGCATGGCGCGCCGAGGGGCTGGC  
 AGGGCGCGCGCGCGCGCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAAGTCCGCGAGGTCTCT  
 GCCCCAGATACTCTGCCCAACCGCACGGTCACCCGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAAAAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCCTTCTGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GATAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCATCTGGTTC  
 GGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTGATTATCTTGCG  
 TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTTGACTGTAACATACTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAAGGTGTGTTTATCCTAAGT  
 CACTGCAGGCCCAACACAGTCACAGCGCTGAAGCAGGAGCTGTTGACATGCGACCTCCGCTT  
 GAATTGCCGCTTTCTCATGACTCCATCTCATCGCCAAAGTTGTGTTGAAGGAGACAGCCT  
 TCCTTTCCAGTGATGGCTTCATATATTTGATCAGGACATGCAAGTGTTTGGTATCCAGGATG  
 GGAGATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGAAAAGAACATGATTCAACA  
 TGCTCCTTTGTTGCAAGTGCCTTAACCTTTCTAATATTCAGCTGGATCTACTGGAATGT  
 GGGCTGTCTATGTCAGACCAACCTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCTGCACGTAAGTCTCCTCCAGAGAGGGTGGTAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTTGGCAGGCATTAAGTGCATATCTGCAGTGTACGCGGAACACCTTGGCAGTGG  
 GATATATCCCGGAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGCAGATGATGATTATTCTCGCTGTCAATGATGCAATGATGCTACAGAGTCTTTAT  
 ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATGTGAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTCGAGTAGGATTGTCAGTGTCTTCAGCGCATTTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTTATTCAACATATTTACCCAAATATTGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTTTCGATTATGGGAGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAATACATTTTCGAGTCTGGCCTAAAGGTATGTTACATTTCTGCAATCATTT  
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTTCAGGAAGATAGGTATTTGCTTTTGCTACTGTTTTAAAGAAAACCTA  
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGGCCTTTGATTCCCTTT  
 CTTACATAAAAATATCAGAAATTACATTTTATACTGCAGTGGTATAAATGCAAAATCTAT  
 ATTGTTACATGTGAAAAAATTTTATTGACTTAAAGTTTATTATTGTTTTTTGCTCCT  
 GATTTTGAACAAATAAGATGTTTTTCATGGGCCCCATAAAGTATCATGAGCCTTTGGCAGTCG  
 GCCTGCCAAGCCTAGTGGAGAAAGTCAACCTGAGAACAGGTGTTTAAATCAAGCAAGCTGAT  
 ATCAAAATTTTTGGCAGAAACACAAAATATGTCATATATCTTTTTTTAAAAAAGTATTTCA  
 TTGAAGCAAGCAAAATGAAGCATTTTTTACTGATTTTTAAATTTGGTGTCTAGATATTT  
 GACTACACTGTATTGAAGCAAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCAATT  
 TTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG  
 TACTTTATTCTGTCTTGTCCCTCAATAATATCACAACAATATCCAGTCAATTTAATGGC  
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGTTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

15/249 15/249 15/249

**FIGURE 16**

MEPPGRRRGRGAQPPLLLPLSLIALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSLELAQVLPPDTLPNRTVTLILSNKISELKNGSFGSLLERLDLRNNLISSIDPGA  
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT  
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT  
 SHRQVVFEGLSLPFCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPEVVNNKGDFRWPRTLAGITA  
 YLQCTRNTHSGSIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELDGVMVDIASNIMLA  
 DERVLWLAQREAKACSRIVQCQLQRIATYRLAGGAHVYSTYSPNIALEYVIKSTGTGTMTCT  
 VFQKVAASDRDTGLSDYGRDPEGNLDKQLSFKCNVSNFTSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560

**FIGURE 17**

GCGTGGGG**ATGT**CTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAGGAGAGAGAGAGATGTTATGGCAAAGGATCTCAAAA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATGGCAAAGGATCTCAAAA  
TCAT**TGAC**TTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
AATAAAGGACAGTGGGTATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTGGAAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

1002003.122301

**FIGURE 18**

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

10020063.121304

CTGTGCGTCTTTGCTTCAAGCCGAGCTCGCCACTGTGCTGCCTGAGGTGCTCTTACAGCCCTGTTT  
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGTCAAGACC  
GCTGCCATGCGCAGTGACGGTAACCCGACACCACATCACAAACCACCAGACGTATCTTCGGG  
CCTGGGGTCCCCCATGATCGTGGGGTCCCCCTGGGGCCCTGACACAGCCCTGGGTCTCCTTCGC  
CTGTCTGACAGTGGTGTCTACCTGCGTGGCCTTCTCGTGGTGGCTAGCGTGGGCGCCTGGAG  
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCCTGATCA  
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
ATCACCTTGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
CTATGTCCAGTTCCTGTCCCACGGCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGAGCCGGGCCCGGCCCGCGAG  
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
CATCATCTTCGCTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGGCCTGGAGTGGT  
GCGTGGCGGTGTACGCCATCTGCTTCATCTAGCGGCATCGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGTACCCATCCCCTTCCCAGCTTCTCTGCGGGCTGGCCTTGTGCTC  
TGTCTCTCTATGCCACCGCCTTGTCTCTGCGCCCTCTACCAAGTTCGATGAGAAGTATG  
GCGGCCAGCCTCGGCGCTCGAGAGATGAAGCTGACGCCGACGCCATGCCTACTACGTGTGT  
GCCTGGGACCGCGACTGGCTGTGGCATCTGACGGCCATCAACCTACTGGCGTATGTGGC  
TGACCTGGTGACATCTGCCACCTGTTTTTGTCAAGGTCTAAAGACTCTCCAAGAGGCTCC  
GTTTCCCTCTCCAACCTCTTTGTCTTCTTGGCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
TCCGCTTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCACCTTTTTCTTTCTTCTCC  
CAATTCTTGACACTCAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTTCTCTTGTGT  
TTCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTT  
CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTACTCTGTGGCCAGGCTGGAG  
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAGCGATTCTCCTCC  
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT  
TTCCACTCTTCTTTTTTCTCACTCTTTTCTGGGTGCCTGTGCGCTTCTTATCTGCCTGT  
TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA  
CCCACCTCCAAGGTGCTGAGCTCACATCCACACCCCTTGCAGCCGTCATGCCACAGCCCC  
CCAAGGGGCCCCATTGCCAAGCATGCCTGCCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC  
GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCT  
CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAAAAACATATATATATAT  
ATTTGGAGGTGAGTAATTTCCAATGGGCGGAGGCATTAAAGCACCACTTGGGTCCTTAGG  
CCCCGCTGGCACTCAGCCTTGCCAGAGATTGGCTCAGAAATTTTGGCAGGCTTACAGAACAC  
CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATCGCTTTCATCCCAACTATTCT  
CTGTGGTATGAAAAAG

**FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPPSFSLGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYVYCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFKV

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21



[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSP LSSLAQVNLSFFSHPKVHMDPNYCHPSTSLHLCS  
 LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSSLCSLEDGLGSPARLASQLLGDE  
 LLLAKLPPSRESAFRSLGLEAQDSLNSPLTESCLSPAEEEEAPCKDCQPLCPPLTGSWER  
 QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

10020063-121304  
 10020063-121304

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCATACAGCCAGCCCCACCTAATTTTGTTCCTT  
GGCACCTCCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCCTGATTGTAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAGAAATGGGCATAA  
TACAATCTATTCTTGGCCATCAAGGATTGTTATTCTTTAAAAAAACCAATACCAAG  
AAGCCTACAAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGAGGCCATGGAAAAGAAAATCAAGACATAAACACAACAGAACATTGCAGAAGTTT  
TAAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATCCCCCTCCTTTGAATCTACCCAACA  
CAGCCACGGAATAACAGATTTCTCCAGTAACATCAGCAGAGCATTCCTTTGGGCAGTCTAA  
AACCCACATCTACCATTTTCCACAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTG  
ATAGTGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCTTAA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAACCTCTTTCCAA  
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTTGCTTACTCTTGTGGGCTACTTGTGTGTGAAAAAGGAAAAAC  
GGATTCATTTTCCCATCGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA  
ATGACACCGGAACCTTATGATGTGAGTTTGGGAATCTAGCTACTACAAATCCAACCTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC  
TCCACTTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCACTTA  
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAATTAAGTGTACGTGGAT  
TTTTGCAAGGAGAATCATAAAGCAGGAGACCAAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTACAATTTTGGCCATCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTCTTAGTAGAAAAATTTTGTGGAATCAGATAAAACTAAAAGATT  
TCACCATTACAGCCCTGCCCTATACTAAATAATAAAAAATATTCCACCAAAAAATCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATGAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCATCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAACCTCAATGAGAATCATGGT

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
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```
><subunit 1 of 1, 334 aa, 1 stop
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><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNTAEVFKTMENKPI SLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLPQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTDTSFHRRLYDRNEPVLRLDNAPEYVDSFGNSSYINPMDTLNDSA  
MPESEENARDYEMDDIPLPRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

**FIGURE 25**

AACAGGATCTCCTCTTGCAGTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCCAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTTCACTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCAAGAGCACCATTACCCTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGAG  
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCCTCCGCCTTCGTGCGAGAGACCTCTGCTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAGGAAAAAAAAAAAAAACTACTAACCACTGCAAGCTCTTGTCAAATTTTAGTTTAA  
 TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTGCATTTATAG  
 GGTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC  
 GTTGTTTTTTTGTTTGTGTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTTGTTTTGAACTTTTGTGTAAATATA  
 TCAGATCTCAACATGTTGGTTTCTTTTGTGTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTGAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGTGTGATGAATCTACAA  
 CCTATAATAAATTTACTCTATACAAAAA

1022063-121301

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPFSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMLPLNTSIVMPPKNLVELFGKLASG  
RYLPQTYVVREDLVAVEEIRDVSNLGFIFYQLCNNRKSFRLRRDLLLGFNKRAIDKCWKIR  
HFFNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCCAGCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGGGGAGCACCAGTCTGTACGCC  
 AAGGAACCTGGTCTTGGGGGCACCATGGTTTCGGCGGGCAGCCCCAGCCTCTCATCTCTCTG  
 TTGCTGCTGCTGGGGTCTGTGCTGTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCTTGAGCCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCAACCCCTGGGG  
 GGCCCATCACCCCCACCAACTTCTTGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCCGGTCA  
 TCACCCGGCAGAAGCAGAAGGCCCTCGGCCATTACCCATCGTCTTCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCGGGGGCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTTCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACCAGGAAGTCCA  
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGTG  
 AGGGGGCTGTGTTGGCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG  
 GAAGCCCAGGGACCACTGGGTCCCCCGAAAGCCCTGTGCTTGACAGAGTGTCCACCCAG  
 TGTCTAACAGTCTCTCCGGGTGCCAGCCCTGACTGTGGGCCCCCAAGTGGTCACTCCCC  
 GTGTATGAAAAGGCCCTCAGCCCTGACTGCTTCTGACACTCCCTCTTGCCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA  
 GGAATCTTACCAAGTGCCATCATCTTCCCTCAGCAGCCCCAAGGGCTACATCTACAGC  
 ACAGCTCCCTGACAAAGTAGGGAGGGCAGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAACTACTTTTTAAACA  
 GCTACAGGGTAAAATCTGACGACCCACTCTGAAAATACTGCTCTTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGATGTGGGGTATAGGGCATTTAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCGGCCCTGGGGTGAGTTTCTCATCCCGCTACTGCTGCTG  
 GATCAGGTTGAATGAATGGAACCTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGTGGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATGTGCTGGCAGCCTG  
 TGTCCACAATATTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
 AAAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 29191, pI: 4.52, NX(S/T): 0  
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGSPPTNFDLGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



**FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
 GGGAGGACAGGGAGTCTGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
 GCAAGGAGGAGACCTTGGTGGGAGGAAGCACTCTGGAGAGAGAGGGGGCTGGGCAGAGATG  
 AAGTTCCAGGGGGCCCTGGCCTGCCTCCTGCTGGCCCTTGCCTGGGCAGTGGGGAGGCTGG  
 CCCCCTGCAGAGCGGAGAGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC  
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT  
 GGTCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGGAAGCAGCCCATG  
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCTTCGACACGGAGCA  
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCTTGGCCACAGTGGTGCTTGGGAAACTTCTGG  
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG  
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT  
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC  
 TCAGGAGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGCT  
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC  
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAAACAATGGCAGCAGCAGTGG  
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGT  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA  
 TCCAGCACCGGCTCCTCTCCGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACCC  
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTACAGGCTTCA  
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGA  
 GGCTCTGGAGACAATTATCGGGGGCAAGGCTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT  
 TGGTGGAGTCAATACTGTGAACCTCTGAGACGCTCCTCTGGGATGTTTAACTTTGACACTTTCT  
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAACAAGGACCAGAGA  
 AGCTCTCGCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACT  
 CCCTCCTTAAACACCAACCCTCTCATCTACTAATCTCAGCCCTTGGCCTTGAAATAAACCTTA  
 GCTGCCCCACAAAAA  
 AA

1002005.124301

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
AGSKVSEALQGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM  
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
GSQSGSSSGSGSNGDNNNGSSSGSSSSSGSSSSSGSSSGSSSGSSSGSGSGSRGDSGSESSW  
GSSTGSSSGNHGGSGGNGHKGCEKPGNEARGSGESGIQGFGRQGVSSNMREISKEGNRL  
GGSGDNYRGQSSSWGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
RSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## FIGURE 31

GACCGGTCCTCCGGTCTCGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG  
 TGCCCTGGGTGGTGGAGTTTCTCTCCTTTGCTGACCATTTGTTCCCTTGCTGGAATATACCGGGACATCTTCA  
 CTCTCTGCTGGCGCTGCACCGGAGCTTGGTGTTCGCGAGGAGAGTGAAGGAGAGTGTCTTCTGCAACAGC  
 TGCTCTACTTGTCTGTCTGGGTGGCTTTTCCAGATTCCCAAGTCCCTGAGGACTTGTCTTCTGGAAGAGG  
 GTCCCTCATATGCTTTGAGTGGGACACAGTAGCCCCAGAGCATGGCTTGGACATCCGCTCTGCTGGACACAGC  
 AGCTGCTCTACACTGTGTCGCCCTACATCGGAGAGCTCCGGAATCTGCTGCTTGTGGGTGTACGGCAGTGTG  
 GACGGAGTGGGGGCTTCATGAGGAAATCACCCCCACCTACCCAGCCTGGGAGCCAGATCTGGTGGCGCAGG  
 GCCAGGGGCTGCAGGCACAGCTCGCCAGGCGCTTTTCCACAACAGCCGCGCTCTTGGCGCGGACCGTAGAT  
 TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAAAATATCAAGGCTACACTGGTGCGAGATCTGGTGGCGCAGG  
 CAGAGTCACTTCTCCAAAGAGCAGCTGGTGACACAGGAGAGGAGGGGGAGAGCCAGCCAGCTGTGGAGATCT  
 TGTGTTCCCGAGCTGTGCCCTCACGGGGCCAGGCATTTGCCCTGGGGCGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGAGCGCTTCTGAGCAGTGCAGAGAATCTGTGTGGGGC  
 TTGCAACAGAGAAGCCTGTGCTTGGCTGTGAGCCACATCACAGCACTGATCAGGAGGAGGTGAAAGCAGCAG  
 TGAGTGCACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCCGAGC  
 GTGCTCTCCTTGGCGCTGGGGCCACGGGACCTGACGAGGAGTCTCCCGAGAGCATCTGGAACAGCTCCTAGGCG  
 CAGCTGGGCGAGAGCTCGGCTGCCGCCAGTTCTGTGCCCACTGCTGAGCAGCATCTGGCAAGTGTCTGTG  
 GACTTAGCTTCCCTCCTCTGTTGAGATCAAACTTCTATCTTAGGGCCCCCGCACAGTACAGTACAGCTGGAGAGGG  
 CAGSCTCGAAGSCTTCTGCACATCTGTCTTCTTGTGGAAGGAAGACTTTCAGGGGCGGCTTCCGCTGCAGCTG  
 CTGCTGACGCCCAAGAAATGTGGGCTTCTGGCAGCACAGAGCCAGGGAGTGGGACTTGTCTGCTATTCTTCTGA  
 CGGGAGCTGGTGGAGAGGGCTGTATGGGACGGATGAGATAGAGGCTGCCTGGGAGCCTCCACAGGCCCCAG  
 TGGCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTTTCTAGCCGAGGCCCACTGCCAGACCTCAC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAGTGGCC  
 CTGCTCTGGGCATTGCACAGAACCTTGACCCCGCTCACAGGAGGCCCAAGTGCCTAATGCAGACCTCAC  
 TGGTTGGGTGTAGCTGGGTCTACAGTACAGCTTCTGCTCTAAGGGTGTCACTGCCCTGGCATTCCACAGCGGA  
 ATCCTTAGAGGAAGGAGCTTGGCTGATTTGGGATTTATGCGAGAAATCTCCAGAGTCTGGAGTGAAG  
 GAGGTGGTGTGTGTATCTTGGATCTAAATGAGATGAGGTGTGTGGGCTTCTCAACACAGAACTCAAGCCT  
 CATTGCTATCCAGCATCTCTAAAACCTTGTAGTCTTGGAAATCATGACAGACAGAACTCTGCTTTAAC  
 TTATGAAGAAAGTTAAACATGAACTTGGGAGTCTACATTTTCTTATCACCAGAGCTGGACTGCCATCTCCTT  
 ATAAATGGCTAACACAGGCGGGTCTGGTGGCTCATGCCGTGAATCCAGCACTTTGAGAGGCTGAGTGGCGG  
 GACTGCCCTGAGGTGAGGAATTCAAGACAGCCTTGCCCAACATGGCAAAACCCATCTCTACTAAATAAAAAAA  
 TTATAGCTGGGCATGGTGGTGTGTGCTGTAAATCCAGCTACTCAGGAGGATGAGGCGAGAGACCTGCTTGAAC  
 CTGGAGGTGGAGGTTGCAGTGAAGCCAGGTGCGACCACTGCACTCCAGTCTGGGTAAAGAGGCGAGACTTCTAG  
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCACTGAAACCTGACTTTCCCGCTGTACCTTCAGCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCTCCTGACCAGGACCAAGCAGAGGCAATTGAGCTTTTTAGATATAA  
 CTGGTTTCTTTTAAAAAAGGGCTTTTATTAATAATCTCCCAACAGATGGCTCTGCAATCTGCCACAGCTG  
 TGGGCGGTGCTCTAGGGAAGGCGCTTTTCCCTGAGGCGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG  
 GCGCTGCTTGGCGGCTCGGCTGTGTCTAGCTGCTTCTTGGCGGCACAGAGCTGCGGGGTCTGGGGGACCGG  
 AGCTAAGACAGGCTCTGTGTGACGGGTGGAGGCTGTCTTCAACCGACACCTGAGGTGCTCTGAGATGCTG  
 GGTCCAGCTGAGTGGCAGCGGGAGCAGCTGTGGCGGTGCTCTTCTAGCGAGCTCTGGGGAACTAAGCTG  
 GGGCGCTCTTGTCAAAGACCGAGGATGGGTGGTGTGGGGACTCATGGGGAATGGCTGAGGAGCTACGTGT  
 GAAGAGGCGCGGTTTGTGTGCTGACGGGCTGTGAGGCGCTCTCTGAGCTCAGTTTCCCTTCCGCTTA  
 ATGAAGAATCTGCGCTGCTGCTCAGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACGAGCGTATG  
 GTTATTTTCAAACTGTCTGCGAGCTTGGCTGGGCACTGGAATGGCCATGTCCCTCTGCTGGCTGGAC  
 CTGCGGCTGGGAGTGGCGAGCGAGGCGGGGCCAGACGTGCGCTGGGGGTGAGGGGAGGCGCGGGGAGG  
 CCTCACAGAAGTGGCTCCCGCACACAGGCGAGGCGGGCTCCCGCGCGCGCCGCCACCCAGCTCCAGG  
 GSCCGTAGACAAGTGGAGTGGCGTGGGCTGCTGCGAGAGGTAGCCCTTGATGAGCTGCGGACGCGG  
 TCGTCCGACGCTGGAAGCAGCGCCCTCCACAGCAGCAACAGCGGCTGGCGCT

10020063.124301

**FIGURE 32**

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
 SLRRTVEFVAERIGSNCVKHIKATLVADLVROAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
 IRREVKAASRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

10020063.121301

TCCCTTGACAGGCTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGAACAGGAAACTC  
 AAGACTCTCTGCTTTTGGCCACAGAGTTCTCTGCAGCTTCTCTTGAGGTGTGAACCCAGATCTCC  
 TGCCCCAGGGGCCACCTGTCAGAGCAGCGGCACACCTACCCCTCAGCAGACGCCCGGAGAGA**ATG**  
 AGTAGCAACAAGAGCAGCGGTGACAGCTGTCTGTGATCTCTTTGGCCCTCATACCATCTCT  
 CATCTCTCTACAGCTCCAACAGTGGCAATGAGGTCTTCATACCTACCGCTCCCTGCGGGCCGTA  
 CGCGCCGACCTGTCAACCTCAAGAAGTGAGCATCACTGACGGCTATGTCCCCATTCTCGGG  
 AACAAAGACATGCCCCCTCTGGTGCACAGCTGTGTGATTGTCTGACAGCTCCAGCCAGCTTGC  
 GGGACCAAGCTGGGCCCTGAGATCAGCGGGCTGAGTGTACAATCCGATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCCTTACCGCGCTGTGTGGCCCATTC  
 AGTGTGTTTCCGGTGCTGTGAGGAGGCCCGCAGAGTTTGTCAACCGGACCCCTGAACCCGTTC  
 CATCTCTTCGGGGCCCCGAGCAAGATGCAGAAGCCACAGGCGACCTCTGTGCGTGTGATTC  
 AGCGAGCGGGCTGTGTTTCTCCCAACATGGAAGCATATGCCCTCTCTCCGGCCGATCGCG  
 CAATTGTGACGACCTCTTCGGGGGTGAGACGGGCAAGGACGGGAGAAGTCTATTCTGTGGTT  
 GAGCACACCGCTGTGTTTACCATTGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATCTCTAT  
 GCATGTGTTCCCCCAACTACTGACAGCGGCCGCCGCCCTCCAGCGCATGCCCTACCACATC  
 TACGAGCCCAAGGGGCCGAGCAATGTGTCACTACATCAAGAATGAGCACAGTCCGCAAGGG  
 CAACCACCACCGCTTCACTCCAGGAAAAGGGTCTTCTCATCTGTGGCCGACGTCTATGGCA  
 TCACTCTTCCCAACCCCTCTCGGACC**TAG**GCCACCACCGCTGTGGGACCTCAGGAGGTGAG  
 AGGAGAAGACGCTCCGCCGAGCGCTAGGCCAGGAGACCTCTCTGGCCAAATCAAGGCTTC  
 CTGGAGTGTCTCCAGCAAAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAAATCAGGGCC  
 TGGGGAATCTGTTTGGCAATCAGGAATTTGGGAGTTTGGGAGTCTATGTGGTAAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTCTTGAGTCAATCTG  
 AGGCTAAGGACATGCTCTTTCCCATAGGACCTTGGTTGAGAGCTTCCAGAACTGGACCCCCA  
 ATACTCCCCACTCTGTCTGGATAATGGGTCTGTGCCAAGGAGCTGGGAACTTGGTGTTG  
 CCCCCCTCAATTTCCAGCACAGGAAAGAGATATGTGTGGGGGTAGAAGCTGTCTGTGAGGCC  
 GGCCAGAGAATTTGTGGGGTTGTGGAGTTGTGGGGGGCTGGGAGAGTCCACAGGTTGGGA  
 GGCTGGCATCCAGGTCTTGGCTTGCCTTGACACTTGGACAAACCCCTTCCCCCTCTCTGGG  
 CACCCTTCTGCCCAACACAGTTTCCAGTGGCGGAGTCTGAGACCTTTCCACTCCCCATGGA  
 GTGCCCTCGGGTGTGCTCTCCCCGTGTGACCACTCCAGGCATATCCCTTGCCTGGAAGGCT  
 CAGCTCTTTGGGGGGTGTGGGTGACCTCCCCACCTCTTGGAATACTTTAGGTATTTTTCG  
 GCAACTCTCTCAGGTTTGGGGACCTGAGGAAGAACGGGACAAAACCTTAAGCTGTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCTCCCTTTCTTGCCCT  
 CTAGCAGGAGGAGTTTTCACACTGTGGAGGCCCTTTGGGGCTTGGCTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGCTCTCCCTGCAGCCTTCTGTGCTCTGGGATGGCTGTCTGGGAGCTGT  
 ATCAGCTGGGTGTCTGTCCCTGGCTCTGTATCAGGCATATTTAAAGCTGGGCCCTCAGTGG  
 GGTGTGTTTGTCTCTGCTCTTCTGGAGCTTGGAGGAAGAGGCTCTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGGACCATGGAGGAGGCCAGCAGCTAGCCATTGTACAGCAATAAACACACCTACGC  
 GGGCGGTGACTGCCCCAGACTTGGTTTGTGAATGATTGACAGCAATAAACACACCTACGC  
 TCCGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

**FIGURE 34**

MSSNKEQRS AVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
 GNKTLPSRCHQCIVVSSSSHLLGTLGFEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
 SSVFRLRRPQEFVNRTPETVFI FWGPPSKMQKPQGS LVRVIQRAGLVFPNMEAYAVSPGRM  
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPLQRPYH  
 YYEPKGFDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

102006-12101

[illegible]

**FIGURE 36**

MLRGTMTAWRGMREVTTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP  
 RMNVTWRLNGKELNGSDDALGLVLIHTGLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPEAQTIIVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRRLS  
 RRALRVLMSGPEDEGVYQCAENEVGSAAVAVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASPPQSSSQPDHGRSLPPEAPDRPTISTASE  
 TSVYVTWIPRNGGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPSRPYVVSIGYSGRVYERPVAGFYITFTDAVNETTIMLKWMIIPASNNNT  
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNMV  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVTGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAWSKQKHTTDLGFPRSALEPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK  
 SSPDEGSFLYTLPPDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPFPFHSG  
 PPCCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



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**FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817  
 ><subunit 1 of 1, 487 aa, 1 stop, 2 unknown  
 ><MW: 53569.32, pI: 7.68, NX(S/T): 5  
 MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS  
 ALTTPLGTTPTGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
 TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
 QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTTCSTPWAESSTKFRHHMYTNVSGLT  
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
 LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV  
 STYPLVIEELLRSXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQGLSTSCH  
 SHLPVQNGHQATHLEVTKQPTNRVFWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein: .****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCAGAAAGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTGTCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
 TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTCCTCCTT  
 CTCCCTAACTTTAGAAATGTTGTAAGTGGCTATTTTGATTAGGGAAGAGGATGTGGTCTCT  
 GATCTCTGTTGCTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGCCAGAAGGGA  
 ATGGAGACATTCGAGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
 CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGAAGATAAAGCTGGGTCTTCA  
 GGAAGTCACTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTTTCTGCAGTG  
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGCTGCACTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
 CTGCTGCCGGTCCCTCACCTGCACCTTGAGGGGTCTGGGCAGTCCCTCTCTCCCCAGTGT  
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCACTGCATGGA  
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG  
 TTTTATTCTCTCA

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**FIGURE 41**

AGCGGGCTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAAACAAATCTGCAAGCCCCGCGACCCAAAGTGAGGGGGCCCCGTGTTGGGGTCTCTCC  
 TCCCTTTGCATTCCCACCTCCGGGCTTTGCGTCTTCTCGGGGACCCCTCGCGGGGAGATGGCGCGCTTGATG  
 CGGAGCAAGGATTGCTCTCTGCTGCTCTCTACTGGCCGCGGTGCTGATGGTGAGAGCTTCACAGATCGGCAGT  
 TCGCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCCCTGGTCAGGC CGCCATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAGAAGGGGCAAAAGCTGGGGCAGGCCTAACCTTTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCACCAAGGATCATCGGCTGCATGGTGTGTGCGAGA  
 AAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCGAGTACCCGCTGCAATTAATGGCATCTGTATCCAGTT  
 ACTGAAGAGCATCTTAACCCCTCACATCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCGAGTCTATTAC  
 TCAAAACCATGACTTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAGGGCATGAAGGA  
 GACCCTGCTACGATCATCAGACTGCATTGAAGGGTTTGTCTGTGCTCGCTATTCTTGAGCCAAAATCTGCAAA  
 CCAGTGTCCATCAGGGGGAAGTCTGTACCAACACGCAAGAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
 TGGCACTGTGCGAAGGGCTGTCTTGCAAAAGTATGAAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG  
 TGTCAAGAAATTTGATCACCATTGAGGAACATCATCAATTGCACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGAAATTAAGGTT CAGATGCAGAAGATGGCTAAAAAAGAAACGTGATAAGAAATATAGATGATCACAA  
 AAGGGAGAAAGAAACATGAATGAATAGATAGAAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACCTTGCTCTGTATAAATAATGTACACATTTGTGGAAATGCTATTATTAAGAGAACAGCACAGTGGAAAT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTCAGATGTCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTTGTA  
 TACAATAGGTTCTAAAAATAAATTTGCTAAACAAGAAATGAAACATGGAGCATTTGTTAATTTACAACAGAAAT  
 TACCTTTTGATTTGTAACACTACTTTCTGCTGTTCAATCAAGAGTCTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAATAATTTGCAAAATAATGGCCAGTGTTTAGGAAGGCTTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAAGCAAAAAACAGTTCC  
 TCCAGATTCCTCAGGAATGCAGATATATCTCTTTATCCTATGTGATTCTCGCTGTAATGCATTATATTTTCCA  
 AACTATACCCATAAATTTGCTAGATGATAAATACTTACACAGCAGAAATTTTACAGATGGCAAAAAAATTTTAAA  
 GATGTCCAATATGTCGGGAAAGAGCTAACAGAGAGATCATTATTTCTTAAGATTTGCCATAACCTATATTTT  
 GATAGATATATGTTGTAATAATCATGTATTATACATACTCTGCTGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGAGTAAAGCAAGAAATTTGGGAAATCTTTTCGTTTGTTCAGGTTTTCGCAACACATAGATCATATGCTG  
 AGGCACAGTTGCTGTCTCATCTTTGAAACAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATATATATTATGCTCAGATGAATTCAGTGTGAGTCTCTCTCCTACTACTCTCCAAATTTATTTATTTATAG  
 TGTGAGATCTCAAAATATCTCAATTTTCAGGAGTTTACAAAAATGTAATCTGAGTAGACAGAGTATGAGG  
 TTTCAATGCGCTCTATAAGCTTCTGACTAGCCAAATGGCATCATCCAATTTTCTCCAAACCTCTGCAGCACTG  
 CTTTATTGCAAAAGGGCTAGTTTCGGTTTCTGCGGCCATTGCGGTTAAAAAATATAAGTACGATAACTTTGAAA  
 ACTGCAATATGCTAATCTATAGACACCCAGTTCCTAAATTTCTTGAACCACTCTACTACTTTTTTAAACTT  
 AACTCAGTTCTAAATACTTTGTCTGAGGACCAAAACATAAAAGGTTATCTTATAGTCTGACTTTAACTTTT  
 TTGCTTTCTGCAATATTTTTCTTTATTTGTCACCTTTTAAAAATTTATTTTGAAGTAATTTATTACAGGAATG  
 TTAATGAGATGTATTTCTTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGATATATTTGCAAGCTATTGAC  
 TTTGTAATTTAGGAAAAATGTATAAAGATAAAATCTATTAATTTTCTCTCTTAAAAACCTGAAAAAATAA  
 AAAAAAATAAATAAATAA

**FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRC  
NN  
GICIPVTESILTPHIPALDGTNRHRDRNHGHSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKFVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

10020053-727301

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCAGCTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTAGATTATAGGTTTTAACATACCTTGTGAAAATACTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTGTGTTCTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTGGAGAGCTTGACACCACCAAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAAGTGAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCTCT  
 CCTGGTTTGGAGTCTTTCTTCCAGGCCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCAGCAGCAGCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGCGGATACCCCAAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCACTACAGAACTCCACATATACAACCTCCGTATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC  
 AGAGTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGAAAAACACCAAGTTGGTCAATGGCTCATTCGTTAAAGAGCAGCCCTTTTGTCTTTTGT  
 TTTTGGACCAAGTGTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAACTC  
 TGCTCTACTATAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGGTGCTGTAATCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

105063-14304  
 105063-14304

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSVLSQLSQRQQHQSQA VTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
GTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

**Signal peptide:**

amino acids 1-24

1002003. 121301



CCGAGTGGGACAAGCCTGGGGCTGGCGGGGCCATGGCGCTGCCATCCGAATCCTGCT  
TTGGAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGACG  
ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
GTCCGCTGGAGTCAACGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA  
GGTGTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGCACGTGT  
GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG  
GTCCCGCACGACCGCGGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA  
CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCCTTTGAGCGCGGTGACT  
TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGAAGGAGGCACTACTCTGCCACCTGCAC  
CACCATTACTGTGGCTGCACGAACGCCGCTCTTCCACCTGACGGTCGCGGAACCCACGC  
GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG  
ACCCCACTGGCGCGCGGCCACAACGTATCAATGTCATCTCCCCGAGAGCCGAGCCAC  
TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCACTCTGATGTTGTCAC  
TGTCCTCTGGCGCGCCGACGGCGCGGAGGCTACGAATACTCGGACCAAGAGTCGGGAA  
AGTCAAGGGGAAGGATGTTAACTTGGCGGAGTCTGCTGTGGCTGCAGGGGACCAGATGCTT  
TAGCAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
GCAAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCGCAGCTGCACCTCTCCTGTCTGTGCTC  
CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCCTTTCT  
GGAATTTGGCTGGGCGTATGCAGAGGCGCCTCCACCCCCCTCCCGAGGGGCTTGGTGGC  
AGCATAGCCCCACCCCTGCGGCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC  
AAAATCCCACTGATGCCATCATGCCCTCAGACCTTCTGGGCTCTGCCGCTGGGGGCTG  
AAGACATTCTGGAGGAACTCCCATCAGAACTGGCAGCCCCAAAACCTGGGGTACGCCFCA  
GGGCAGGAGTCCCACTCTCAGGGCTCTGCTGCTCCGGGGCTGGGAGATGTTCTGGAGGA  
GGAACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
CCTCTGGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
GCACCATCTGTTCTCCCGAGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCTAGCCTTG  
CTCTCAGCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT  
GGACTCTGCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA  
CAGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT  
GCATCTGCTGTTGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA  
AAAAA

**FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWRQPPGVPHDRADRLDL  
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPPPRGSPGNSSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDLDKGFRKENCK

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

1002063.12331

**FIGURE 47**

CGCCGGAGGCAGCGGCGCGCTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT  
 CAGCACAGTTCAAACCTCCACCTACGGAAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCGCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTACGCCTGGGCAATTGGCAGTCTACTGCCATGGAACCTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
 GGACCCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCTGGTGGCCAACCTTCTGCTTGTCAACAGGGTTGCAGTCCGATC  
 CGTGCTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATACTGGTCACTGGTGA  
 GTGGGACACTTCTCCTGGACCCGTGGTTTTTTTTGGCGTACCATTGTCTGCATGGTGATCC  
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG  
 AGGAACTCCCAAGCACTGATATCAGGAGGACCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCTGTTCTTGGCGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA  
 GGACTCCCTCAGTGCCCTTCCGGTGGCCTCCAGATTCAATTGATTTCCACACACCCCTCTCC  
 GCCCATTCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGCACCTACGCTCTTCTTCATCACC  
 AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT  
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGG  
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTTTCGTGCTCTGTAACACAGCCCGCGT  
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCTCCTCAGCGGCTAAGATTGTGCCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTCACTCCTGGTGCACCTCATCTTAGAAGGGAGGACAAGGACATTGGTG  
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAGGCC  
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACTCGGGCCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCATGCCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAACAGAACACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCACGCTGCGCTCATTCCAGCT  
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCTTGAATGGA  
 AGTCCCTGGCATGGTCAGTCCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACCTGCCACTAACCAGACTGGAAGAACCCAGAAAGATGGGCCTTCCATGAAT  
 GCTTCATTCCAGAGGGACCAAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
 TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
 GTATTCAAAA

**FIGURE 48**

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLRPEDRFCGTYIIFFSLGI  
 GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
 LLLSRLEYARYYMRPVLAAHVFSGEEELPQDSLAPSVASRFIDSHTPPLRPILKKTASLGF  
 CVTYVFFITSLIYPAVCTNIESLNKGGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
 305-330, 448-472

1002003.121304

**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGTGTACCAAGAGCTGGAGACACCA  
 TCTCCACCGAGAGT**CATG**CCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCTCC  
 TCAGCCTGGTGGCTCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGAACCTGGGGCTCAATCGGACCT  
 GAAGCCCCAGAGGTGATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGACCAGAAACAGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCAACC  
 AGTACGACAAGAACAGCTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAG  
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGCCGCGCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCGCTGCCCCGCCACATGCAGGAGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCGCGAGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGCGGCCACTCAAACACCGATCGCCGTCGCGCATGATTTTCTACCCGCCG  
 CGCGGAGGGCGCTGCTGCTGGCCTCGTACACGTGGTGGACGCGCGCGGCGAGCGTTGCGC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTCTGTGCCAGCTCTGGGACGGACCGGCGTCTGCAAGCGTTGGGCGGAGGACAGCACA  
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGA  
 AA

**FIGURE 50**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQIETSPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

1002003004005006007008009001000

## FIGURE 51

CTGACATGGCGCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTCTGGGCGGCCCTCTGCCTGCAT  
 GGACGCTCTGAAGCCACCCTCTCTCTGGAGGAACACGAGCAGGGGAAGGACAGGACTCTGTGTGGCAGGAA  
 GAACCTCAGAGCCGGGAAGCCCCATTCTACTAGAAAGCACTGAGAGATCGGCCCCCTCGCAGGGCTGAAATTTCCCT  
 GCTGCTGTTCCAAAGATGCTTTTATCTTTAACTTTTTTGTTTTCCCACTCTCCGACCCCGCGCTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTCTTGTGGCTGATCACCAGACCTCAACCCGCTCTTACCTCTCTTGACCTTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGCGAAGGGGGTTTCAGAGAAGAACAAATGACCTAACAAAGTTGCTG  
 CTTCTCAGATGCCAGACTATGTCTGAGGTTTTCCAAAGAGGACTCGCTGTCTGACAAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTTACAAACAGCTGTCTGATAGACAGAGTACCTGGGTCT  
 CTGTCTCTTGCATAAAGGTTATAAATCATCACCAGACCAAGTTTGTCCGCACTCTTGTCCAGAAATAGGCCAGAGTG  
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGAGC  
 CATCGTACATATTTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAGGCAATTTGGTCTGAT  
 AGGGAATTAGAGAAAGGCTTCAACCCGAGGCTTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAAAGAGGGGAGAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCCAAAGAGCACTTCA  
 AAAACCTGTGCCTCTAGCCCCAGAAGACCTGAGCGTCTATCTGCTTCAACAGTGGGACCAAGAGTGAACCCAAAGG  
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTTGAAGAGGATTGACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTTGTTTCCCGCGGTGCCCTGACCTCTTAAACAGGATCTACGATAAGGTACAAAATGAGCCAAAGACACCCCTT  
 GAAGAAGTTCTTGTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAAGCTCATCTTTGCAAAAGATCCAGGACAGCTGGGGCGGAAGGGTTCTGTAAATTTGCTACTGGAGC  
 TGCCCCATGTCCACTTCACTCATGACATTTCTCCGGGCAGCAATGGGATGTCCAGTGTATGAAGCTTATGGTCA  
 AACCAATGCCAGCTGGCTGTACATTTACATTTACCTGGGAGCTGGACATCAGTCACTTGGGTGCCCTGGC  
 TTGCAATTACGTGAAGCTGAAGATGTGGCTGACATGAACCTTTTACAGTGAATAATGAAGGAGAGGCTGTCAT  
 CAAAGGTACAAAGCTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGCAACAGGAGCCCTGGACAGTGTAGGCTG  
 GCTTACACAGAGGACATTTGGTCTGCTGGCTCCGAAATGGAACCTCAAGCATCATGACAGTAAAAAGAACATTTT  
 CAAAGTCCGCCACAGGAGATACATTTGCCACAGAGAGATAGAAAATATCTACAAACAGGAGTCAACCACTGTTFACA  
 AATTTTGTGACAGGAGATAGCTTACGGTCACTCTTGTAGTAGGACTGGTGCTTCTGACAGACATGACTTCCCTC  
 ATTTGACGCAAGCTTGGGCTGAAGGCTCCTTTGAGGAACTGTGCCCCAAACCAATTTGAAGGCAAGCCATTTT  
 AGAGGACTTGCAGAAAATTTGGGAAAGAAAGTGGCTCTAAAACTTTTGACAGGCTCAAGGCCATTTTCTCATCC  
 AGAGCCATTTCCCTTGAAGATGGGCTCTTGACACCAACATTTGAAGCCAAAGCAGGAGAGCTTTCCAATACTT  
 TCGGACCCAAATTGACAGCTGTATGAGCACATCCAGGATAGGATAGGTAAGTACTTGAATACCTGCCGGCCACTG  
 TGCAGTCTTGTGAGAAAATGGATTAAAAAATATTCTTACATTTTGTGCTTCTCCTCCTATTTTAAAAAC  
 TGTTAACCTCAAAGCCATAGCTTTTGTTTATATTGAGACATATAATGTGTAACTTAGTTCCCAATAAATCA  
 ATCCTGCTTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTATCAACATGCTCTGTCTTCA  
 GATCCAGTTTATGTTCTGTGCTCCTTCTCATGATTTCCAACTTAACTACTATTAGTAACCAAGTTCAGGGGT  
 CAAAGGGACCCCTGTGCTCCTTCTCTTTGTTTGTGATAAACATAACTTGCCAAACAGTCTCTATGCTTATTACA  
 TCTTCTACTGTTCAAACATAAGAGATTTTAAATTTCTGAAAACATGCTTACAAATCATGTTTCTAGCCACTCCAC  
 AAACCACTAAAATTTAGTTTATGCTTATCCTCATCATCTATGATCATATCTATGAGACAAATGTCCTCGGATGCTT  
 CTGCGTAAATTAATTTGTACTGAAGGGAAGGTTGATCATACCAACAACTTCCATAACTCTCTAGTTAGATA  
 TCTGATCTGGGAGTATTAATAATTTGGGCTATGACATCTGTCCTGAGGAAAGGAACTGCTTCTTAAAGCATTTATTA  
 CAGTAGGAAGCTGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
 GGTGGGCGAGTGAACCTTTTCAGTAAATGAAGCAGCACTGAATAAAAAACCTCTTGAAGCTGGGAACAAAGATCT  
 ACAGGCAAGCAGATGCCACCAACAGGCTTATTTCTGTGAAGGAACCAACTGATGCTTCCCCACCCCTGGATT  
 AGAGTTCCTGCTCACTTACCACAGATAACACATGTTGTTCTCACTGTAAATGTAAGCTTTTAAAAATAAC  
 TATTACAGTAAAAAA

10020053.121304

## 111 12 •



**FIGURE 53**

GGAGGCGGAGGCGCGGCGAGCCGGGCGGAGCAGTGAAGGCGCTAGCGGGGCGGAGCGGGG  
 CCCGGGGCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGT**AT**GGACGACTGGAAGCCCGAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACAGCGGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGCGGTGCTTTTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGAGAGCCCCACGGCCAGAGGCACTGGTCCCGCGCGGTCTGTGAGCGTAGA  
 GGTGTATTCAAGTCGACGCAAAATATATGTGGCAGTGGATGGCACCCGCTGCGGAGATG  
 AGGCCCGGAGCAGGGCCGGGGCATCCATGTCTATTGTCTCAACAGGCGCGGGCCACGTC  
 ATGGCAAAACGTGTGTTTGACACGTAACCTCATGAGGATGAGGCCATGGTGCTATTCTCT  
 CAACATGGTAGCGCCCGGCGGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCGCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCGAGAGTGCCACTGGGCAGACAGAGCTGAACCGTCGCCCGCGGCCG  
 TTCTCGACGAAAGTTGAGGGCTATGGAAGTGATGCGACTCAAGAGCCCAACCCATCCGACG  
 GTTCAGCCCTGACCCACTCCAGACAACAGGTCTCAATGTGCTGTGGCTGTCATTGCGAG  
 GGAACCGACCCAATTACTGTACAGGATGCTGCGCTCTCTGCTTTCAGGCCAGGGGTGTCT  
 CCTCAGATGATAACACTTTTCTATTGACGGCTACTATGAGGAACCCATGGATGTGGTGACCT  
 GTTTGGTCTGAGGGGCTCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCACTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGTGGTGCTC  
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCGGAGAGTGATCATCCTGACG  
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC  
 TACTTCAAGAAGCACAAGTTCAACACGGTTCACAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGAAGTTACAGGCTGCTCACTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTGGAAGACTCTTCTGCGCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAAGTGCCCTCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCTGGTGGTGGGGTCCCGGCTTCCCTTACTCAGTGAAGAAGCCACCTCAGTC  
 ACCCAATTTTCTGGAGCACCCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATGA**GACTCTCCTCCAGGACCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACTTGTTTTTAACA  
 TGAGACTTAATTACTAACTCAAGGGGAGGGTTCCCTGCTGCTCAACACCCCGTTCTGAGTT  
 AAAAGTCTATTATTACTTCTCTTGTGGAGAAGGCGAGGAGTACCTGGGAATCATTAGC  
 ATCCTAGCAGCTCATCTGCGCTTTGAATACCTCACTTTCCAGGCGCTGGCTCAGAACTCA  
 ACCTATTATTGACTGCTCTGAGGGCCTTGAACACAGGCCCAAGGGGCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
 CAACCCATGGACAGGCCACGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA  
 GACACTGACCAAGGCTCTCTCAGCCTTCTCTTTGTCCAGATTCTCAAAGCTGGATAAGTT  
 GGTCAATTGATTAATAAAGGAGAAGCCCTCTGGGAAAAAATAAAAAAAAAAAAAAAAAA

1002005.121301

**FIGURE 54**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKILIDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDEVEYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGD PVLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLRLRLSLLSAQGVSPQMITVFIDGYEPEMPDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDAQGYEHTA
EDPALLYRVETMPGLGWVLRRLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHS
KNPCEDSLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVGRGNHRLWRLFRKKNH
FLVVGVPASPYSVKPPSVTPIFLEPPPKEEGAPGAPEQT

```

**Important features of the protein:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC  
 CTGTTTAAAGAACTAAGACCACTTTAAAGCCACTGGAAATTTGTTGCTAGTGGTTGTTGGGTGAATA  
**AAGGAGGGCAGAAATGGATGATTT**CATCTCCATTAGCCTGCTGCTCTGCTGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACACGATGAAGCTGGTGACTGTTTGG  
 GTGCTGGCCTTCTCTGTGGAACAGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA  
 GATATTTCTGAGGGAAAAACCAACCAAGCAAGTGAACACATATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCCATGACATGAGCACAGCCAGCACCACACAGCTGCATGCCATATATTTGGTG  
 TTTCCCTCGTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCATGTGCATTTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTTCTTCTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCACTTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGCAGCAGTAAAGAAAGCCCTTTCAGAGGTGAACGCCACGGGATGG  
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA  
 ATAGGGCACAGCCACAGCCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCTTGGAAAGTGGCAGCCCT  
 GGTTCCTGGGTGCTCATCCCTCTCATCTGTCAGTAGGACACCAGCAT**TAAATGTT**CAAGGTCCAGC  
 CTTGGTCCAGGGCGTTGCCATCCAGTGAGAACAGCCGGCACGTCAGCAGTACTCACTTCTCAGTC  
 TCTGTCTCACCTTGGCCTCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTTG  
 AGTAATGGAAGGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTTCTTAAACCTATTCTCAGGGAAGATG  
 GAATTTAGTTTTAAGGAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTCTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
 AACATGGTCTCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATCGGTTGATGGAAGGTGATA  
 GCACCCACTCACTTAGATGCTAAGGTGATTCTAGTTTAACTTGGGATTAGGGTCAGGAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCCTTTGGCACGTGCCCTCTCTGAATCCAGCCTGCCATTCCATCAAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCCTGTCAAGTTCTCCTTTGCAGAA  
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCTTCAAGAA  
 CAGTCAGATCACAAAGTGCTTTGGAAATTAAGGGATATTAATTTTAAAGTATTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTGTTTTT  
 TTTTTTTTTAATATTTCTCTAGCAGATCAGCAATCCCTCAGGGACCTAAATCACTAGGTGAGCTTT  
 GGCACACTGTGCTCTCTCACATAACCACTGTAGCAAGATGGATCATAAATGAGAAGTGTITGCCATA  
 TTGATTTAAAGCTTATTGGAATCATGTCTCTGTCTCTTCGCTCTTTCTTGTCTTTCTCTCAACTTT  
 TCCCTCTAGCCTCTCCTCGCCACAAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAAT  
 CTTATCAGGACACACCACTCTCTCGAACTGTAAATGAAGATAATATATCTTTATCTTTATCCCCCT  
 CAAAGAAATACCTTTTGTGTCAATGCGCGCTTTGTTGAGCCCTTAAATACCACTCCTCATGTGTGAA  
 ATTGACACATCACTAATCTGGTAAATTTAAACAATTGAGATAGCAAAAGTGTTTAACAGACTAGGATA  
 ATTTTTTTTTCATATTTGCCAAATTTTTTGTAAACCTGTCTTGTCAATAAGTGATAATATTTGAT  
 TATTAATTTATTTTACTTTCTATACCAATTCAAAAACATPACACTAAGGGGAAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGAGCTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCATG  
 ATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGAAGGAAGTAGCAAAATAGGATACAGTTGTATGTAGTCAATGGCAACAATGTCATACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACATATATGGTTGCCATAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAA

1020063.321301

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFFVMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTGLVHVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

100005.12101

**FIGURE 57**

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGGCGGCCCTCGTAGCGGGGCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGAGGGCGGCTGCAGAGAGAGGCGCGGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCTGCGAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAAACAGCAA  
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGAGGAG  
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGCCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAACTCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACCCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
 TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAATGTACATCTGA

1020063.121301

**FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQT PAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

1002003.121301



**FIGURE 60**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
```

```
<subunit 1 of 1, 1089 aa, 1 stop
```

```
<MW: 118699, pI: 8.49, NX(S/T): 2
```

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MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPFPGSLPWGSQKPGKACW
MASRFSRVVLVIDALRFDFAQPHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPFSFNVRDLTDVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGHHPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAAFLYSPAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFSGGEDSQPHSSALAAQASALHLNAQ
QVSRFLHTYSAAQTQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCICLLASQWAIISPGFPFCPLLLTPVAWGLVGAI
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA
VFFSDSFVVAEARATPFLGGSFILLLVVQLHWEGQLLPPKLLTMPRLGTSATNPPRHNGAY
ALLRGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRRLRVLVSGASMVL
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGLERTKSQGLPTVAAYQLGSVYSAMVTALTLLAFPLLLLHAERISLVFLLLLQSF
LLHLLAAGIPVTTGPPTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFILGIQILACALAASILRRLHLMVWVKVFAPKFI FEA
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR
```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

10020057 1230



TGCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGAGACGGGCAGTTCCCTGT  
GTCTCTGTGGTTTGCTTAACCTGCAACATCACCTTCTTATCCATCAACATGAGAAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
TCATCACAAATTGGCCCCACAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTGT  
CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
ACACGTGGAGTCCCTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
CCAGGACTTTGAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
CCCATACTATTACCGTGTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
GTTGGCAGAGAGAACACCCAGCAAATTTGATTTTGATTTATGGAATGAATTTGACAAAA  
GATCTTTTGTGCTCTGAGTGAAGAAATCGTGATTAACCTTATCACCTTCAATATCTCGGATGAT  
TCTAAATTTGTCTCATCGGATATAGTTTACTGGGAAAAAGCAGTGATGATCCAGCCTTAA  
TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGAGGGAAGAGGAGGTGAAACATTTAG  
GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
CTCACCCAGCAAGAGTCCCTCAGCAGAACATACCCCGGATAAAACAGTCATTGAATATGA  
ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTGCAGG  
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCG  
CAAACGTTACAGTACTCATACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC  
AAACTGGCAGGCTGTGTATTCCTTCGCTGTCEAGCTTCGACCAGGATTACAGAGGCTGCGAG  
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGT  
TATATGTGCAGATGGAACATGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAC  
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAGAAGTGTTCCTCAGT  
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTATTCTCATAGCAGGTGTGTGATTG  
GTTTCATGCATGTAGGCTCTTAACAATGATGGTGGGCTCTGAGTCCAGGGGCTGGCGGT  
TGCTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATCAGG  
TGGGTGT

MSYNGLHQRVFKELKLLTLCSSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPPPRAQPSKEQ  
CARTLKDQSSSEFAKAKIIFWVYLPISITVFLFSVMGYSTIYRIYHVGEKHPANLILYGNFED  
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSLLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLRTIPPDKTVIEYEDVRTTDCAGPEEQELSL  
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD  
PQGTQLRCIPSLSSFQDSEGCEPSEGDGLGEEGLSLRYEPPAPDRPPGENETYLMQFMEEW  
GLYVOMEN

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCT  
GATGCTGCCCGTGAAGCCCCCGCAGGCTCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGTGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGTTGTTGCTGGGCGCCACGTCTGAGTACTGCGGAGCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGGCCAAGGTCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCTTGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGAGGGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCTCGTTTCTTCTCGGGCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCTTTGTGGCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCTGCTGGGACACACAGGCCCCCGAAGGAGGCCCTTGAGCCACAACCT  
TGGCGCATGCAAAATGAGATGGCCGCTCCAGGCCGTGAATGTTCCGTGCTGGGCCCCAGGG  
AGGCTGATGTTCTAGGTTGGGGTGGGACGGGCGCGGTGGGGCGACCCCATTCACATGCA  
AAGGCGAGAGCAAAACCCAGTAAATGTTAACTGACAAAAAAGAAAAAAGAAA

**FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 30350, pI: 9.66, NX(S/T): 2  
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDRLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHEMTHANDIC  
LLRLNGSAVLGPAVGLLRLPLGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLLTLMCLTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30

1020063:121301

**FIGURE 65**

GAGCTACCCAGCGCGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCGGCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG  
 CAGGCGCCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAAACACAGGCATCGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCTTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAGCCGCGCTACT  
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGCGCGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGCGGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCGAGCTGGCCGCGCCAGCCAGCACATACTGGCCGTGGCGGAGGAAC**TGG**CGGATGTT  
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCTCCCCAGAT**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG  
 ACCGAGGACAGCTGTCCGCATGCCCGAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGCGCCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGAAGTGGC  
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGTTCCGCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCAGTCAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGATGCATGGTCTCTCTGAGCCTTGGTTTCTTTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGACAGGTGCAGGTGTATCCC  
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGCTGCTACAGGACCTGGGA  
 TTGCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC  
 TTGCTCATTT

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALRLARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNVNARHLDLASLKSIREFAAKIIEEEERVDILINN  
AGVMRCPHWTTEGDGFEMQFGVNHLLGHFLTLNLLDLKLKASAPSRIINLSSLAHVAGHIDFDD  
LNNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSPELAQFSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW  
AESARLVGLEAPSREOLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCCTCGGGACAGGAGACCCAGAAAGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCTTGGCGCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT  
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAAATCCGAGCTCTGAAGG  
 ATGGCTATGAGAGGTTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGAGCAGCAAGG  
 GCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGCCTGGCCGAGGTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAGATTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTACAGCCTGGTTCCAGCCCACTCTACAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATCCAACGCCTACCTGCTGCTCAGCCCATCCGGAAGGAGGTCACTCACCTGGA  
 GCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
 CCACCGCATTTGCTGCCCTCAGAGCCTTGATGTCCGGCCTCCCTATGCAAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGCCACAGCCTTCACTATGCCAACTCAGCGTGGCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTTGGTGGGAGATAAGTGGGTGGCCAAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCTTGCAGCTCCAGCCCTGAAGACT**GTA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAATCAGAGGC  
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTGACAGTAGGATGCACAGTACAAGAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
 AGTCTCAGATCACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGT  
 TTTTGGCACTTTGAACCTTGACCACAGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCCAAGACTTAAAGACTTTCTCCCCACTGCCTTCTGCTGCAGGCCAAG  
 CAGGAGTGTCCCCCTCCCAAGAAGCATATCCAGATGAGTGGATACATTATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
 ATGTTTATAAATCAAAA

10020063.124301

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVHSLSEASINIRALKDGYEKVF  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRSGYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLYKERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVLTNHRIAALTGLDVRPPYAEYLQVNVYIGI  
GHYEPHFHDATSPSSPLYRMKSGNRVATFMIYLSVSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSSEGGSDTLHAGCPVLVGDKWVANKWIHEYGOEFRRPCSSPED

amino acids 1-19



**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAAACCGCGCGGGGAG  
 CGCCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGCGCTGATTGGGGCCCTGGTCTCT  
 GTCTGTGGGCATCTATGCAGAGGTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCTTCC  
 TGGTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCTGAACGACAACATTGGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA  
 AACATCATGGACTTTGTTGAGAAAAAGTTCAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCTTACA  
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTCTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGTTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
 TCCTGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
 CCCAGGGAGCAGAGCCTGGGGCTCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGTTATCAA  
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCCTGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGTAGCCTA  
 GTTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTGTACAGATAACAGGAGTTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCCAACAGTGTGTAA  
 TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

1020067.123304  
 1020067.123304

**FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AII LILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVI IW FMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

1002003.121301

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAGATGCGCCGCGCCGCTGGACCTTCACCCTTCTCTGTGGTTTGTGTCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTGCACTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAGCCAGCCGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCTGAAGCACATCATCTGGCTGAAGGTCAACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAATGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTCT  
 AGCTCTACCTGGGGGCAAGTTGTTGGACTCACAGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCACCCCTGGACAACATCCCGTTGAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTTGG  
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCTGTGTCGGAACCAAGATGGCAAATTAAGATCTGGGGTCCAGTGTCATTGGTG  
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCTCTACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAACACTTGCCCTGTGAAAAA

1000063.121301

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
```

```
><subunit 1 of 1, 484 aa, 1 stop
```

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFHTLLCGLLAATLIQATLSPTAVLILGPKVIEKELTQELKDNHATSILQQLPILLSAM  
REXPAGGI PVLGSLVNTVLKHHI IWLKVITANILQLQVKPSANDQELLVKIP LDMVAGFNTPL  
VKTTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQIYL  
GAKLLDSQGKVTWKFNNASAALTMPTLDNIPFSLIVSQDVVKA AVAASVLP EEFMVLLDSVL  
PESAHRLKSSIGLINEAKADLGSTQIVKILTQDTEFFDIGHGAKVAQLIVLEVFPSS EAL  
REPLFTLGIEASGEAFYTKDGLILNLNISSDRIQLMNSDIGQVDPVQLNKIITEI IHSIL  
LPNONGKLRSGVPVSLVKALGFEAESSLTKDALVLTPASLWKPPSPV SQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

**FIGURE 73**

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTGCAGCTTCCCTCAGCCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCACTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCGGTCGCCTTGTGAAAGCCCCACCAGAAATTAATCCGTTATCGTCATGTTCACTGCT  
 CTCCAACATGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATCCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTGCCATGGTGGATTG  
 CTGAAGGCCTGATGATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTATCATCAACTTT  
 CCTGCAAAAGGAAACCCAAACGGGGTGATACATATGAGTTCAGGTCGGGGTTTTCTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAAGCTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTTGGCTGTTATTTGGTGGACTTGTGTAT  
 CTTCCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGT  
 GCTGAAACACACATTTGTTCTTCTGTTTAATGGTGGAGTTACCTTAGGAATGGTCTTTTATG  
 TGAAGCTGTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAGGTCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTGAAAAGAAGATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCCTA  
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATATAAAAAATGTAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACACTACTTAGTTAACTTGGTCACTGTAT  
 TTTATATTGCCCTTATCCAAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC  
 TGTACAGATAACTACATTAGGAATTCATCTTAGCTTCTTCACTCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTTCTTTTGTAGTAGAGAAATATGTGTGTCATGTGGTCTTCTGAAAATG  
 GAACACCATTTCTCAGAGCACAGCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGATTTAGAAA  
 GATTTAGATTCTATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAA  
 TAGCTTAGTGCTAAAAATCAGTGTAACCTATACATGGCTAAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAACCCCGTCTCTACTAAAAATAT  
 AAAAAATAGCTGGGTGTGGTGGCAGGAGCCTGTAACTCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTCAGGAGATGGAGTTTCACTGAGCCGAGATCAGCCCATGCACTAC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAA

1002063.121301  
 1002063.121301

**FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

10020063-121301

**FIGURE 75**

AAGCAACCAAACTGCAAGCTTTGGGAGTTGTTGCTGTCCTGTCCTGCTCTGCTAGGGAGA  
 GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGGTACCGGGC**GATG**CTA  
 TCGCTGTGGGTGTCTGGTGGTCGACGCCCTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA  
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCTGAGCGACTCCCTTCGATG  
 GAAGGTTAAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG  
 ACACGTGGGACTTCCTTTCTGAAATGCCCTACACAAACTCTCCAATTTGTTGCCCATCACGCGC  
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAAATAATTTTAAGGGTCTAG  
 ATCCAAATTATACAACATGGATGGATGTCACTGGAGAGGCATGGCTACCGAACACAGAAATTT  
 GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG  
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAAACAGGA  
 CTAAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA  
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTACTTGGGATTAAATTTACACACCCC  
 TTACCCCTTACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTACACATCTCTTTATT  
 GGCTTGAAAAAGTGTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTGAGAAATG  
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCATGGAAGATTTACAAAAAAGA  
 AATTAAGAAATATTAGAGCATTATTATTATGCTATGTTGCTGAGACAGATGCCATGCTTGGTG  
 AAATTTATTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACATTGTCATATACTCCTCA  
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG  
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCCGGCCCTACAAGTATCAAAATG  
 TGGTTTCTCTTGATATTTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG  
 AACCTGAGTGGATACCTCTTGTGGCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT  
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCCTCCA  
 CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTGCGATGGTGCATCAATATTG  
 CCTCAACTCTTTGATCTTTTCCCTCGATCCAGATGAATTAACAAATGTTGCTGTAAATTTCC  
 AGAAATTACTTATTTCTTGGATCAGAAGCTTCATTCCATTATAAATACCTTAAAGTTTCTG  
 CTTCTGTCCACCAAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAAGGAACCAAGGAAGTA  
 TGAAATGCAATTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTT**TGA**CAAAAAA  
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT  
 AAATGAACAGATTTTAAATAATTACCAAGTTTGGCCGGGCACAGTGGCTCACACCTGTAATC  
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCATCTCGGC  
 CAACATGTTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCTGGCGCGGTGGTGCACA  
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG  
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCG  
 AAAAAAATAAAATAAAATAATAATAATACCAATTTTCAATTTTGTAAAGAAATGATG  
 TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAAATGGTTATTATTTA  
 GGCCTTTGTACAATTTCTAACAAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAAATCTGTA  
 ACAGTTATGTTCCGTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAT  
 AGTTGTATGTGAGCATTGTATGGTGAAAAA  
 AA

1020053.724304

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRILTFHPSQVVKLPFINF  
 MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
 KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDQNTDKAVNW  
 LRKEAINYTEPFVIYLLGLNLPHYPSPSSGENFGSSFTHTSLYWLEKVSHTDAIKIPKWSPLS  
 EMHPVDYYSSTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
 SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPIKAGLQVSNVSLVDIYPTMLDIAGIPL  
 PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
 ILPQLFDLSSDPDELTVAVKFPETIYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
 QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAY

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
 498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

1002005-121301



**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATC**  
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCCTTCTGGGGCTTTTGGGCACACT  
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCAGAGCCAAAGACAGAGTGGCGGTAGCAGTGGAGTCTTTTTC  
 ATCCTTGGAGGCCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
 ATGTGT**GTA**AAGAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTGCACCTTGCTGCTC  
 CCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG  
 ACTGACCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCGAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

1020063.124304  
 1020063.124304

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886  
><subunit 1 of 1, 230 aa, 1 stop  
><MW: 24549, pI: 8.56, NX(S/T): 1  
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGGLLGFIPVAWNHLGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCS  
SQNRNSYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**FMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCCTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTCGCTCCTGC  
TTATGTGTCACTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG  
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTTCCTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

1002005.721304

**FIGURE 80**

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

10020063.121301

**FIGURE 81**

CTCCACTGCAACCAACCCAGAGCC**ATGG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCTGACCTTCATGGTGAAGCTGATAAACCAGAACTGCCA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGC**TAA**TGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCTGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTCACCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

10020067.121301

**FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

1000000.000000

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCGCTCCCGGCACCAGAAGTTCTCTCT  
 GCGCGTCCGACGGCGAC**CATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGCAGAACGTCACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGCCCATCCGCAACCTCACGTTCAGGACCTTCA  
 CCTGCACCATGGAGGCCACAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGTCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCTCTCTCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGCAGGCAGC  
 CTCGAACCGCGCTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACCC  
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTTCGAGCCACGAC  
 CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCATCCCTGGACCTGTCCCTGACT  
 CTCCAAACTTTGAGGTATCT**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCGTTCGAAGGATTTTGGGGTGTCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTACCAGCTACAGATGCCAAATGACTTACATCTTAAAGAA  
 GTCTCAGAAGCTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCTCCAGGCACAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCGTTTTGGCCGAGGCTGCTTCTGTCT  
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACTGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCGGAACGGGAAGTAC  
 ATGTTGGCCACCCACTGGAGATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 GTGGAGAGGGGCACCTGCCCCCCGCCCTCCCCATCCCCACTCCCACTGCTCAGCGCGGGCC  
 ATTGAAGGGTGCCACACAATGTCTTGTCCACCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLLGPVVK  
GHDVTIFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLASD  
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVVPSSSQ  
DSEINITAAALATGACIVGILCLPLILLLVYKQQAASNRRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDVPVDPSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

1002003-104304



**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTCC  
 TTTCTTGCCACCGCTGCTTCTTGCCCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTCTCCTTTTTCGTCTCCCTTCTCCCCGA  
 CTCCGCTCCCGGACCAGCGGCTGACCTTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTTC  
 TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGCGCAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTAAGTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
 TGTACC GCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC  
 AGCACAACGGGACCATGTACCAACCGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC  
 CGCTGCCCAACCAAGTGTGTCTCTGACAGTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
 AACCTGCCCCGAACAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGACGTGCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGC  
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCAAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
 ACCCTGCGGTACCCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGGACAAA  
 GCAGACCTTGGCCACAGTGAAGTCAAGTCTACCAAGTGTCCCAAGGCACCGGGCCGGGTCT  
 CGTCCACACATCGGTATCCCCAAGCCAGACAACTGCGTGCCTTTGCCTTGGAAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGTGGTAAAGATGAGGAAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAACTCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTGCTGGCCCCCAC  
 GAAGTCACTGGAACGTCTTCTAGCCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTTATATATTAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

1020057.12304  
 1020057.12304

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQC VLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDFC SSDAGRKRGP GTPAPTGLSAPLSFIPRHRFPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRFALEHEASDLVEIYLWKL V  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERG TALPTARWPPRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

1002005-12301

**FIGURE 87**

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC  
GTGGGCGCTCCGCTGGCTGTGCAGGCGGCC**CATG**GATTCTCTGCGGAAAATGCTGATCTCAGT  
CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG  
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG  
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
CGTGCCCTGGAGGAAGAACTGGATGGTTGGCGGC GAAGGCGGCGCCAGCGGGAGGTCACCG**T**  
**GAG**ACCGGACTTGCTTCCGTGGGCGCCGGACCTTGCGCTTGGGCGCAGGAATCCGAGGCAGCC  
TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG  
TCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCAAACCCTGGACTGACTGCTTTAAGGT  
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCCGATGTGGTGAAGTGAAGAACCAATAAAA  
TCATGTTCTCCAA  
AAAAAAAAAAAA

10020063.424304

**FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18

10020063 121304



**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWSGGLQGQHHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDGTYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFPFAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ  
QWDTPCPRENAEAAFVICGLTYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

1005003.121304

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCACAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCAGTCCCTCGGCTGGTTCCTCCCGGCCACAGCGAAGTG  
 GAAAGGTCACAAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGCGGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTCGGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAACCTCCC  
 ATAGTCATCTGCCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 TGAAATG**TAGG**GATGAATCACATCCACATTTCTTTAGGGATATTAAAGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAGGTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFRPTAKWKGPQQLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELEDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQSFSQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRNLNGEHLTYFTLNPRFISVFFRPTPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTSNESSSQATTFFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

1002063-14334



**FIGURE 93**

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACCAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
 CATAGGAGGACCTGCCGAGCCTGGCGGCGCTCGCCCTGTTGTCTGCGCGCCGCGCGCGCGCG  
 CCGTGCCTCAGCCGCTCGCGGGGAATGTCACCGGTGGCGGCGGCGCGCGGGGAGGTG  
 GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTAGGGCGACGGC  
 TCCACGGGCCAGGCCCCGAGGACCGGGCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCAGTCCCCGGAGACACCCCTCTTTGGGCGACTGCTGGACCCCTCTCC  
 ACCACCTTTAGGCGCGCTCGGCCCTCGCGGACCACCCCTCCGCGGCGGGAACGCACTTC  
 GACCACCTCTCAGGCGCCGACGAGACCCGCGCCGACCACTTTTCGACGACCACTGGCCCCG  
 CGCGGACCAACCCCTGTAGCGACACCGTACC GGCGCCACGACTCCCGGACCCCGACCCCG  
 GATCTCCCCAGCAGCAACAGCAGCGTCTCTCCACCCACCTGCCACCGAGGCGCCCTC  
 TTCGCTCTCCAGAGTATGTATGTAAGTCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
 TGCAAGAGGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGACCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGGAACTGAAGTTTATT  
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAAATTTTATATACCTTTTATCTCTTACTTTATATGT  
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCAGCTAG  
 AGTCGCAATTTTTCTCTGGGATAATTTCTGTAATTTTATGGGAAAAAATTTATGAAGAAT  
 AAATCTGCTTTCTGGAAGGCTTTTACGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTGGTTTATTTTTCTCTCTA  
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCATTTTA  
 TTTAAGTAGTGGTAAGTAGACTGGTTTTACTCTATTACCAGTACATTTTGTAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGA  
 ATAATGTACTGTTATCTAAGCATTGCGCTTGACTGCACTGAAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACCTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTATACTAGTGAACCTGGGTATAACCCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTTGGCAAGTAATTTCCCTTCACTGAGCTTGTCTCTCTCAAG  
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGTTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAATGTTTTAAGA  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTTAGTTTATTAAAAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCGCTGTAATCTAGCACTTTGGGAGGCCAAGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGCTCTACTATAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACTGTAGTCCGAGCTACTCGGAGGCT  
 GAGGCAGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGCGCCACT  
 GCATCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952  
><subunit 1 of 1, 258 aa, 1 stop  
><MW: 25716, pI: 8.13, NX(S/T): 5  
MRSILPSLGGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFP PRATA  
PTAQAPRTGPPRATVHRPLAATSPAQS PETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSSTTGPA TTPVATTVPA TTPRTPTPDLPSSSNSSVLPTPPATEAPS  
SPPEEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFY LNYTSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

J03006.121301

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCAACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

105005-121301

**FIGURE 96**

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLR TLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

1020063.121301

**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCTTGGCCCACTAGTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAG  
 GCACCCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC  
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGTGTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTGTCTTCTGCGTCATCTTCTGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGTGTGAGGGGTTGAGCCT  
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCGCTCCCCCAGCT  
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGAT**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAGACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAGACAGACAAATTCCTA

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPYSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNYKHHRLSVNVTALTTHRNILIPGTLESGCPQNLTCSPWFACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLPQPQDHGTSLTQCQVTFPGASVTTNKTVHLNVSYPPQNLMTMVFQGDG  
TVSTVLGNSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSPQSNPGVLELPW  
HLRDAAEFTCRAQNPLGSQQVYLVNLSQSKATSGVTQGVVGAGATALVLSFCVFVVR  
CRKKSARPAAGVGDGTIEDANAVRGASQGPLTEPWAEDSPDPQPPASRSDSVGEGLQYA  
SLSFOMVKPWSRSGQEATDTYSEIKIHR

amino acids 1-15

## amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCTGTTCCCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCTCGAACACTTAGG  
CAGCCCCGGGTCTGCACCTCCAGAGCCCCACCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCTTTCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCAAA

10020057-121304

amino acids 1-17



**FIGURE 101**

GTTCGCAGATGCAGAGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGGTACTCTGTGG  
GGCAGCGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTCCGGCTGGGGCAGCACGTCC  
AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA  
CCCACCACAGCCCATCCCCCTCCATTTCACCTTGGTGTGGTTCCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA  
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amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
 TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCCGAAGAA  
 GTGAAAATAGAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
 ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCAGCCGGA  
 CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTTGGTGTGGGCAAGTCATAAAGGCCTA  
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT  
 TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
 AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA  
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
 GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
 AAACAAAGTCACTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA  
 TCTCCCAATACATTGATTTTGGTATAATAATGTAGGCTGTTTTCGAACTTAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRVVIPPSPFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKKDEKPRD
KSYQDAVLEDIFKKNHDHGDGFISPKEYNVYQHDEL

```

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCTGTGCTAAGTGCCCCCAAATGCTTCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAC  
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

102000.000000

**FIGURE 106**

MQGPILLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

10020000.121301

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG  
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
 CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCCTCACAGCGGCTCACTGCA  
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCC GGCTACCTGGGAGCCTCGACGAGCCA  
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC  
 ATCACCACCCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT  
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
 GTCCCTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC  
 CTGTTTCTCCACCTCCACCCCAACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC  
 AATATCTCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTTCTTGGAACCT  
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
 ATAAATATAAATGAAGGAGGGGCACCAAAAAAAAAAAAAA

1002005.121301

**FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLQLCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSSGGLVCGGVLQGLVSWGSVGPCQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

1082003-121301



**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCCGCGCAGGAGAGAGGCTGGCC  
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCCGAGATTGACC  
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCTACCGAGACTTTGTGAA  
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCCTGA  
 GGACCCCGCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCTCATTGTGTTTGGTCATTGAGGTTTGTGTTGTTT  
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC  
 TGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
 ATATCAAACCAAACTAGAGGGGCGAGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTTCAAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
 CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACC  
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
 TACCAGAAGGAACCCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGCTTCGGAGGCAGAAGTGAGGCCTG  
 GGGTTTGGGGGAAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN  
NEGEIDLMSLKRMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSVCLKVM  
MFEGKANESSPKPVGPPPERDIASLP

10020063.121301

CGCGCTCCCCGCGCGCTCTCTCGGGCTCCACGCGTCTTGCCCGCAGAGGCAGCCTCTCTCCA  
GGAGCGGGGCTCTGCACACATGCGCCCCGGGTGGGAGAGGGTTCGCGCGCCGCGGTGCGCGCG  
CGCTCGTGGCTTGCCCTTGCGCTGGCGAGGCTCTGAGTGGGCTTCAGCGCTGCGCTGCGCTGCC  
CACCAGTGTACCTGCTCCGCTGCCAGCTGGACTGCCACGGGCTGGGCTCTCCGCGCGGTTC  
CTCGGGGATCCCCGCAACGCTGAGCGCTTGACCTGGAGCAAGAAATATCACCAGGATC  
ACCAAGATTGACATTGCTGGCTCAGAACCTCCAGGCTTGTCATCTGGAAGACAAACAGGT  
CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGAGCTCGCGCTGAACA  
AGATAAGCTCGAAGTCTCCAGAATTGCTTTCCAGAGCAGCCGAGCTCACCAGATC  
GATTTGAGTGAACACAGATCGAGGGGATCCGAGGAGGCGTTCGCGGCATCACCAGTGT  
GAAGAACCTGCAACTGGAACAACAACCAATCAGCTGCATTAGAGTAGGAGCTTCCGAGCGC  
TGCGCGATTGGAGATCCTTACCCTCAACAACAACAATCAGCTGCATCTTGTTACACAG  
TTCAACCATGCGAGATGCGAAGCTTGGCGCTTCACTCCAACCCACTCTACTGCGACTG  
CCACTGGCTGGCTCTGCGATTGCTGCGCAGCAGCGAGCAGTGGCCAGTTACACTCT  
GCATGGCTCTGTCATTTAGGGGGTCTCAACGTTGGCGGATGTGCAAGAGGAGGATCGTGT  
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CCATCCAGACACTCCACTTAGCCCAAAACCCATTGTGTGCGACTGCCACTTGAAGTGGCTG  
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ACCTCTCAACTCTGATCCTGAGCTACAAACCGGTGAGTGCATCTCCGCTCACCGCTCTCAAC  
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CTCTTTCACGACCTACATCTCTTCTTCACTTGGCGCTGGAAACAACCCACTCACTGTG  
ACTGCACTCTTCGTTGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGAGCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCTCTGCTGCAACCCCAACCCACCGCT  
CCAGTGCAAAAGGCGGAGTGGACATCAACATTGTGGCCAATGCAATGCTTCCCTCAGGC  
CGTGCAAGAAATACGGGACATGCACCCAGACCTGTGGAGCTGTACCGTGTGCTCGCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTC  
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 AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCCTGAGCTGAACCTCTGTGACGATG  
 AGGCCAAGTGCAATCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGAGTGCCGCCACGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG  
 AACACCCCCCCCCATGGTCCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
 GGGGCCAGTGCACTCGTGGTGCAGCAGGAGCCACCTGCCCTGCCACCCAGGCTTCGCCGG  
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
 CCTCGCCCAAGGTCCGACCCAGGCCAACATCTCCTGACGGTGGCCACTGACAAGGACAAC  
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACAGGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGATCAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGCGCCAGGGCACGG  
 ACCGGCCTCTAGCGGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
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 GTGCAAGCACGGCTGTGCCCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
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 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCATCATGGAATGTGCTGGGGCT  
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amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCAACCGACTAGTGGAGCAGTGTTCCTCCGCA  
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
 CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
 CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC  
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
 GACACAAGGAATGAATATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
 AGTGGA AAAAAGGCTGTGAGGTTTCCTTAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
 TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
 TTAAATGTC

1002065.121701

**FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

10020053.121301

**FIGURE 115**

CAGGCCATTTGCATCCCACTGTCCTTGTGTTCCGGAGCCAGGCCACACCGTCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTTAAACTTGTACATGGCTCCC  
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
 ACATTCAAGTCCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCGAG  
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAAATCTCC  
 CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAAGTCCCAAGTCAATTGCTGTTAATTGCGGTGGACCTTGGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAACCTTCTTAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGCTTTTTATGCTATAATCATTCCAAATTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTACGACAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTCCCAGATTCAAT  
 CCACCGAAGTGTCACTGTCACTGTGTAGGGAATTTTGTGTTGCTGTCTTGGCTGGATC  
 CATAGCGAGAGTGTCTGTATTTTTTTAAGATAAATTTGTATTTTGCACACTGAGATATAA  
 TAAAAGGTGTTATCATAAAAAATAAAAAAAAAA

1020063.121301



**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKKILFYCHFDPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

1002003.121301

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAAC**ATG**TTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCGCTGTGGT  
 CTCTTCTGTGGTTTGGCAGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCC'TTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAAT'TGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAAC'TTGGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCAGCTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC  
 TTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCTAGTACTC  
 CTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAAT'TGTGTACCTGGGCAATCTGTTTTTTAAACCACCTCTGAA  
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTCGAAGTCCCA  
 AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTTATT  
 CCTAGAGAGACCCCTCGTCTTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAAC'TTTTCTCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAAC'TGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 AT**TAA**AATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATT'TGTAC  
 TTAA

10020063.124304  
 10020063.124304

**FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVS LGTV DVLKQHINPNKTS DPFETMLKSL LRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGT VWSEIGKGF LDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEE VQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL  
QDPNTWPSPHKFD PD RFDD ELVMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

10020053.121301

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT CAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTACCCGTCTTTGGGCTGAAA  
AAGAAACCCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCTTGGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
ATTAAAAAAAAAAAA

10020053.124301

**FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

10020063.121301

**FIGURE 121**

TCCGGACCCCTGCCGCCCTGCCACT**TATG**TCCC GCCGCTCTATGCTGCTTGCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGACAGTGGGCTAC  
AACTTCCTGATTGGAGAAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTACGGGTGC  
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTATGGGCAACTACATGG  
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACATCTC  
TCAGGGCAACCACTTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC  
CTGCTGATCCGCACTCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAGGAATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSH  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLAGGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

1002005.121301

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
 CCTAGGGTCTGTGGCCCCGCTTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC  
 TGGG**TG**ACCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGCCTCAGGCAGGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGTCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCTCCACACTAAGGCC  
 ACAGCCCATCCGCGTGTGTGTCTCCCTCTTCCACCCCAACCCCTGTGGTCTCTCTGGGAG  
 CATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC  
 CGGATCTGGATGGGCCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGGCCGAGA  
 GCATGTGCTGGATCTGTCTGTGTCTGTCTGTGGTGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTT  
 GCCCCGGGGCA



**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSILYLICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSREPMAN  
STLLGLLAPPGGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA  
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGTAAAGGGTCTGCATGAGCTCCTTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
 TGGTGGAAAGTGTGCGCGCCGCCGCCCTCGTCTCGAGCGCTGCGACCTAGCCGCTAG  
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
 GGCTGCGGGTGCCACACGGCTCACCATGGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA  
 GAAAGGAATTTACAGTTTCAGTTTTACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
 GTTAACTTGATGTTAAATGGAACACAGTAATATCTGCCCTTGCGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGTCTGTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
 AACTGGAGAAAGGTAATTTGGTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG  
 TTCCCCCTATTAGGATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTTTTTCATCATGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
 ACAGTCAAAGCTGTCTGCAAGACTTATCTGAATTTCAATTCCTGGGATTACTGAATTAGT  
 TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGGTTGGTCTCTGTAA  
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
 TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA  
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAGAGTCATATTTTCCAAGTTATATT  
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAGTGGCTTACCCAAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACCTTTATTGC  
 TCAACTTTAATTAATAATGATTGATAATAACCACTTTTATTAATAAACCTAAGGTTTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCTTAACTCTTTAAATGTGA  
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGAATAT  
 CTTGTCTTTTGTATAGGTATATGAATTCATAAAATATTTATGTCTGTATAGAATAAAGA  
 TTAATATATGTTAAAAAA

1020057.747304  
 1020057.747304

**FIGURE 126**

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIFYDQILVNVGNFFTLESVVFVAPRKGISFSF  
HVIKQYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGC  
 TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCT  
 TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
 GAAGAGTATAAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
 CCAGGCACAGTGGGCATTATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGATTTTTTGTGGCTGTGAGAAGA  
 AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
 ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
 ACAAGAACTTCTTCTTTACAACCAGCGCTCCAGATAACCCTCAGGGAACCAGCACTTCCCAA  
 ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTCTG  
 GTGGAATTGAGAAAGAAATAAACTATGCAGATA

10020053.121301

**FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFEMARVIIDN
KDGPTQKYLLIFGAFVSYYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLPGPTVGIGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKLLCQDKN
FLLYNQRSR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 129

CGGCAACAGCCGCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTCGCTCTGGGCTGCCCTTCT  
 TGGTGCTCTTGGTGCCCTCGGTGCAGAGCCATCTGGGGTTCTGGGGCCCAAGAAGCTCTCGCAGAAAGACGCG  
 AGTTTGAGCGCACTACGTGGACGAGGTCAACAGCAGCTGGTCAACACTTACACCTTCAACCTACTGTGACCC  
 GCGACAGGACAGAGGGCGTGGTGCTGTCTGTAACGCTCTGAACAGCAGAAAGCAGAAAGGCGCGCTGTGCTTTTGGG  
 TCCGCGCAGAGGAGGCTGTGGTGCTTCCCTCCAGGTGCCCGCTAATCCTGCAGGGGATGTTTACGCCAAGTACTCT  
 ACCAAAAAGTGGACGAAACCTGTGTGAGCCCCACCAAGAAATGAGTCGAGATTCAGTTCTTCTACGTGGATG  
 TGTCCACCTGTACCAAGTCAACACACATACCACTCCGGTCAGCGCTGCTCAGTCTATCTCATTCAGATGTGCTGTCTG  
 GGGAGCAGTTCAGCTTCAATACCAACAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCTTGAAGSGCTGGACT  
 CGGTAAATTGTCAAGGTGACCTCCAACAGGCCTTCCCCTGCTCAGTCTATCTTCATCTCAGATGTGCTGTCTG  
 TCTATGACCTGGACCAACAGCTAGCCTTCTATCGGCATGTACAGACGATGACCAAGAGGGCGGCATCACCGTAC  
 AGGCAAGAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGAAGCCGAAGACAGGCTGCGGGGGCT  
 CCCTGCCCTTCTACCCCTTCCGAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAACCCCTGTGAGTGTCTGG  
 TGTCTCAAGCAGTCACTGTGAGGCATACGTCACTGGGATGCTCTTTGCGCTGGGTATATTTCTCTCTTTTACC  
 TGCTGACCGTCTCTGTCGCTGCTGGGAGAACTGGAGGCAGAGAAGAAGACCCCTGCTGTTGCCATTGACCGAG  
 CCTGCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCTCTTATGAGGGTTACAAC  
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGTTGACAGCGCTGGCAGCTGGGGACCTCTCTACG  
 GTTACAGGGCGGCTCCTTTGAACTGTAGGTACTCGGCCCGAGTGAACCTGAGCTCTGTGGAGGAGGATG  
 ACTACGACCATGACCGCATGATTCCGACAAAGATGTCTTTCGACCAAGCAATACCTCTATGTGGCTGACC  
 TGGCAGGAGGACCAAGCGGTGTTCTGGCGAAAAAGTACCAGATCTACTTCTGGAACTTGGCACCATTGCTGTCT  
 TCTATGCCCTTCTGTGGTGACGCTGGTGATCACTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT  
 GCTACTACAATCTCTCTGCGCCACCCACTGGGCACTCAGCGCTTCAACAACTCTCAGCAACCTGGGGT  
 ACATCTGCTGGGGCTGCTTTTCTTCTGATCATCTGCAACGGGAGATCAACCAACCGGGGCCCTGTGCGCGA  
 ATGACCTCTGTCGCTGGAATGGATGCCATCCCAACACTTTGGGCTTTTCTACGCACTGGGCAAGCCCTGATGA  
 TGGAGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGGACATCTGTTGATG  
 ACATGCTCGCGGCACTCTGATCTGAAGCTTACCAAGAGCGGCACCGGACATCAAGCGCAGCGCTACAGTG  
 CCTACGCTGCTGGCCATGTCTATCTTCTCTGCTGGGCGTGGTCTTGGCAAGGGAACACGGGCTTCT  
 GGATGCTCTTCTCATCATTCACATCATCGCCACCTGCTCTCAGCAGCAAGCTCTATTACCTGGGCGGTGGA  
 AACTGGAATCGGGGATCTTCCGCGCATCTCCAGCTGCTCTACACAGCTGCACTCGGCACTGCAAGCGGGCGCG  
 TCTACGTGGACCGCATGGTGCTGTGGTCTATGGGCAAGCTCACTCAACCTGCTCCTTTACTTCCGCTCTTACA  
 TCTATCATGAAGCTCCGGAGTGGGAGGAGGATCAAGCTCATCCCCCTGCTGTGCACTGTTTGCACCTCGTGGTCT  
 GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGAGCTCAGCACTGGCAGAAAAACCCCTGCAGATCGAGGAGCA  
 ACCGGGATGCACTCTCTCGACTTCTTTGACGACCAGCATCTGGCACTTCTCTCTCTCATGCCATGTTCTCG  
 GGTCTTCTGTGTGTGTGTGACACTGGATGACGACCTGGATACTGTGAGGCGGAGCAAGATCTATGTCTTAC  
 AGGAGCTGGGCGCTTCGCTTCACTCAAGGGGCGCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTGCTGT  
 GTGGGATGAGTCCGACACCGCTGCCAGCACTGGATGGCAGCAGGACAGCGAGCTTAGCTTAGGCTGGCT  
 GGGACAGCCATGGGTGGCATGGAACCTTGACGCTGCCCTCTCGGAGGAGCAGGCGCTCTCCCTGGAAACCC  
 AGATGTTGGCCAAATGCTGCTTCTCTCAGTGTGGGCGCTTCCATGGGCGGCTGCTTGTGCTCTCAATTT  
 GTCCCTTTGCAAGAGGAGGATGGAAGGACACCTTCCCATTTCACTGCTTGCATTTTGGCCGCTCTCTCCCC  
 ACAATGCCACGCTGGGACCTTAAGCGCTCTTTTCTCCCTCACTCCCATGCCAGGCTTAGCTTGGGGCTGTA  
 ATCTCTGCTCTGATCAGGCGCCAGTCTCTCTTGGGCTGTCCCTGGCTGCCATCTGCCCATTCAGTCAAGC  
 AGGATGGATGGGGGTGAGATTTGGGGTGGGCGAGCTGTCGAGACTTTTGGTGTAAAGGCTGCAAGGGG  
 CTGGGCGAGTGCATTTCTTCTTCCCTGACCTGTGCTCAGGGCTGGCTTTTGAAGATGCGCTCAGGCCAATT  
 TGAGAAGCGCTTCTGATTCAAGAGGCTGAATCAGAGGTCACTCTCATCCATCAGTCCCAAGCATGAGCC  
 AGCAGCAGGATGGAGGAGAGGCGCTCACCCTTCCCTTCTTCTCAGGCGCTTAGTCTTGCCAAACCC  
 AGCTGGGGCTTTCAGTGCAATGACACTGCCAAGATGTCCAGGGGCAAGGATGATACAGAGTGTGCTGTT  
 CCCCTGCTGCTTCCAGCTGTGGGACCCCGATGCTTACCTTAGAAGGGGCTTCAGGAAGGATGTGCTGTTT  
 CCCCTACAGTGGCCACTCTAGCTGCTCTAGGACCCAGGCTGGCTTCTAGTTTTCGTCAGCTCTCAGGCA  
 AGTTCTGCTGTAGTATGCACACATCATATGAAACCTTGGAGTTTACAAGAAATGCCCGCACTTGGGAC  
 CCGTGGACCTGGTCTTGGATCCCTTCTGCTCCACCTGGTCCACCCAGATGTGAGGATGGGCGAGCTCAGG  
 CGGGCGCTCTGTTGGGGATGGGAATGTGTTTTCTCCAACTGTTTTATAGCTCTGCTTGAAGGGCTGGG  
 AGATGAGTGGGTCTGATCTTTTCTCAGAGCGTCTCATGCTATGTTTCCGTTTCTATGAATGAATT  
 TGCATTCAATAAACACACGAGCTCAAAAAA

**FIGURE 130**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPELLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCVPYDLNNAVFIGMYQTMTKKAAITVQRKDFFPSNSFYVVVV
VKTEDQACGGSLPFYFPAEDEFVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACFESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDSL SYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQT VVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGFLYAMGTALM
MEGLLSACYHVCNPYNTNFQFDT SFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSPVWGFALFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGTCTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTCTG  
 ACC**ATGGT**CCCTGCCTGGCTGGCTGCTTTGTGTCTCCCGTCCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC  
 TGACCAAGTTGCCCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGACGGGACTCA  
 GGCAGGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGAGTGAACGATACCAAGGTG  
 CCCCATTCTCTCAAGGCTCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCTGGCATCCC  
 CTTCTCTTCTCTGAGGCTTACAGCCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTCACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCCAGGCCACTG  
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCTCCATAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTCTATACCCGACCCACATGGCCAGGTACACTGGAGTGGGGTGTATGT  
 GCACATACAGCTGGAGGCCATCCCCGGGACCTTTGAAGTGAATGCAGAGGGAACCTCT  
 ACGTGACCCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCTTGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGTGATGGATGAGAA  
 TGACAACGTGGCTATCTGCCCTCCCGTACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGCTCCCCAATTC  
 CACGTTGTGATCTCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTGAAGGGGAGGCCCTCCA  
 GGTGAGCCCACTTCAGGAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGTGCGCATGGACCTGGCAGGGCGAGAGGGTGGCTTCAGCAGCAGCTGT  
 GAAGTCGAAGTCGAGTCACAGATATCAATGATACGCCCTGAGTTTCATCACTTCCAGAT  
 TGGGCCATAAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCTTCCGCCATGAGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCCAGCGTACGAGGCCAGTGTCCCATCAGTGCCCC  
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCCCTCAGGTTCT  
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCAATTGAGAAATTCCTCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGTCTGTGGAGGCCAGGA  
 TACAGCCCTGACTCTTGCCCCGTGCGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCGACGGTCCCTACAGC  
 TTCACCTTGGTCCCAACCCACGGTGAACGGGATTGGCGCCTCCAGACTCTCAATGGTTCC  
 CCATGCCTACCTCACCTTGGCCCTGATTGGGTGGAGCCACGTGACTGTGCTAGTGGAGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC  
 GTGGAGGGGCGAGTGATGCGCAAGGTGGGCGCATGAAGGGCATGCCACGAAGCTGTGCGG  
 AGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCATTTTACACC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCTCGAAGGCC  
 ACTGT**TGA**TGGCCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTTGCTCCATCTGAGTCCC  
 CTGGGAGAGGCCAGCAGCCAGATCCAGAGGGGACAGGACAGAGTAGAAGCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCTGGACACCAAC  
 TTTATGGACTGCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGCCAAATAATAAGGCCCA  
 GAGAAGCTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

10020063.124301



**FIGURE 132**

MVPAWLWLLCVSVQALPKAQFAELSVFENYGGNFFLYLTKLPLPREGAEGQIVLSGDSG  
 KATEGPFAMD PDSGFLLYTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL  
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIIESTWVSLEPIHLAE  
 NLKVLYPHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
 SHGEDYAAPLELHVLVMDENDNVPICPPRPDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
 VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPRLAGQNILLVLAMDLAGAEGGFSSTCE  
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGLVAMLTAIDADLEPAFRLMDFAIERGDTE  
 GTFGLDWEPDSGHVRLRLCKNLSYEAPSEHVVVVVQSVAKLVGPGPGGATATVTVLVERV  
 MPPPKLDQESYEASVPISAPAGSFLITIQSPDPI SRTLRFSLVNDSEGWLCEKFSGEVHTA  
 QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPFYSF  
 TLGPNPTVQRDWRQLQTLNGSHAYLTLALHWVEPREHIIIPVVVSHNAQMWQLLVRVIVCRCNV  
 EGQCMRKVGRMKGMPTKLSAVGILVGTLLVAIGIFLILIFTHWTMSRKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

1002003-721304

**FIGURE 133**

CCGGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTAGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACCAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGAGCTTTCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGCTTTGAAAACCGGCCGATGTATGTAAGTT  
 GAGCACTGGGAAAGCGCTGAGGCGCGCCGCGTTTGGCTGAATGCAGGCATCCATTCCCAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAAATGGATATTTTCTGTGTGCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTCTGACCCAAATAGAACTGGAACGCTAGTTTTCGAGGAAAG  
 GGAGCCAGCGACAAACCTTGCTCCGAAGTGACCATGGACCCACGCCAATTCGGAAGTGGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGAGCTGCTGATGTCATATGGTACTAGTCAAAAAGGCCCAAGTGCAGTGC  
 GAGGAACTGCAGAAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTTCTGTGTGCGGCCTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGCG  
 TTCCTCCTGCCAGCTAACAGATCATCCCACCTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGGACAACTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGGACGCTCCCTGGAGT  
 CGTGTGCTCTGGCGGTGTCCTGCAAGAACTGGTTCGCGCAGCCTGCTCAATTTTGGTCTCTG  
 CTGTTTTTGATGAGCCTTTTGTCTGTTTTCTCCTTCCACCCCTGCTGGCTGGGCGGCTGCACCT  
 AGCATCACCCCTTCTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC  
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTCCTTTAATTTT  
 TCGCAGTCTTCTGGAAAAATATTTTCTTTGAGCAGCAAACTTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTGAGACAGAGTTTGCTCTTTGTCG  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA  
 ATTCTCCTGCCTCAGCTCTTGTAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGGCCACTG  
 TGCCGGGCCGTCCTCCTTTTTTTTAGGCTGAATACAAAGTAGAAGATCACTTTCTCTCAC  
 TGTGCTGAGAAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCAGTGTAGGCTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTCAGGATGGTGAATTTATCCCATCTGCTCCATTTGGGCTTACCTCCT  
 CTTTGCCTTTTGAATCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTCAATCACTCAT  
 CTGGCCTGGATAATCTCACTGACCTGGCACATTTCCATTTGTGCTGTGATCCTGTGTT  
 TCCTTGTCCGTTTTGT  
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCACTG  
 GCCTCTGTTGTTTCAATTCACCTCAGCACGTACCATCTGCTGCTGCTGTTGTGTTGTTGTTT  
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGCTTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

1020063.121301

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFRLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPATISILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDNL

**Signal peptide:**

amino acids 1-16

10020057.121303

[illegible]

**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSFVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGMQRLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

10020063-121301

**FIGURE 137**

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACCG  
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG  
 CCTTTATCTCTTCAACCTTCAAGTCCCCTTTCTCAAGAACTCCTGTCTTTTGCCCTCTAAAG  
 TCTTGGTACATCTAGGACCCAGGCATCTTGTCTTCCAGCCACAAAGAGACAGATGAAGATGC  
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTC  
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCAGCAGC  
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAAGCAGGCCACCATCTCAGGTCCCA  
 GCGTGACCTCCAATGGGGTCAAGTATGTCACCAACTCTGAGTTCACATAACCTCCAGTGGG  
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA  
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
 CCTCCAGTGGGGCCAGCACAGTCAACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC  
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA  
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA  
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC  
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG  
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCCTCCAGTGGGGCCAGCACAGCCACCAAC  
 TGTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC  
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA  
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAG  
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCAACAACTCTGAGTCCAGCACACCTCCAG  
 TGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCA  
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC  
 ACAACTCCAGTGGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGG  
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT  
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCAACAACTCTGAGTCCAGCACAACT  
 TCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAAGGTCTTGAAC  
 AGCAGTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAA  
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCG  
 GCCGTGGGGCTCTTGTCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC  
 CTTTAAACACAGTGTCTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG  
 GGAATCATGGAGCCCCCACAGGCCCAAGGTGGAGTCTCAACTGGTTCTGGAGGAGACAGTA  
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGCCCTTGAGCAGCCCCGGAAGCAAG  
 TGCCGATCTTTCAGGAAGGAAGAGACCTGGGCACCCAGACCTGGTTTCTTTTCATTTCATC  
 CCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCCTCAC  
 TTTCTTGCCCTTTACCAGACACTGGAAGAGAAATACTATATTGCTCATTTAGCTAAGAATAA  
 ATACATCTCATCTAACACACAGCAAAAGAGAAGCTGTGCTTGCCCGGGGTGGGTATCTAG  
 CTCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA  
 TCTCCACAGTAAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAA

10020053.121301

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTNNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSS  
TTSSGASTATNESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNESRTT  
SNGAGTATNESSTTSSGASTATNSDSSTVSSGASTATNESSTTSSGASTATNESSTTSS  
GASTATNSDSSTTSSGAGTATNESSTVSSGISTVTNSESSTPSSGANTATNESSTTSSGA  
NTATNESSTVSSGASTATNESSTTSSGVSTATNESSTTSSGASTATNSDSSTTSSEAST  
ATNESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFRRPVSSIAMEMSGGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

1002005.121301

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAATATGCATCTTGCACGCTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGCGCTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCCTTTCATCAACCTTCCCGCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGTGGGAGAATAATGTGCCGTTGTACATCAGCTGAC  
ATGACCTGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTGTGAATAAACTTGATACACCA

10020053-721301



**FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675  
><subunit 1 of 1, 247 aa, 1 stop  
><MW: 25335, pI: 7.00, NX(S/T): 0  
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

102005.121301

**FIGURE 141**

CTCGGGCTCCCGAGGGGCTCGCTGGCGGGCGGCTCGGCAAGGGGGACAGATCAGTGGACACTCCAGGAAGAGGGG  
 CGCGGGGGGGGACGTACGCTGCGCTGACCGTACTGACTCTACAGTTCGAGAGCGGGGGCCCCGGGGGAGGACTCG  
 GGGGCGGACGCTCGGGGCGGAGCTCGCCGCCGATGAGTCCGGCGAGGCCACTTGAGCCCGAGGCCCGGGACACGGCTG  
 GCTCTGCTCTTCGCA**ATG**CTGGCAACCGATGGGCTCGAGGAGCTGGCTCGGCCGCCACTGGGGGGCGCTGGCG  
 CCTCGGCCACCGCTGCTGCTGCTCTGCTGCTGCTCTGCTGCTGACGGCCGGCTTCGACACTGGGCGGCTCGAGC  
 CCGCGGATCAGCCTGCTCTGGGCTCTGAGACGGCGGCATCTCTCAGATTGGAAGTTCGAACACATCTCAACTAC  
 ACAGCCCTCTGCTGAGCAGGACTCGCAGGACCTGTGAGTGGTGTCTGAGGAGGCCCTTTGACTCAGTACGAG  
 AGCTTCAGCTCTCTCGGACGGGGGATACAGGAGTGTCTTGGGTTGAGACGACAGAGAACAACAGAGTGC  
 AAGCTTCAGAGGGCAAGGCCACACAGCGGACTGTCAAATACATACATCAAGATCTCTCGCCTCAGCGGACATCA  
 CTGTTCTCACTCTGGGCACAGCAGCTCTGACCCCATGTACTACTACTCAACATGAGAAATCTACCCTGGCAAG  
 GACGAGAAGGGGAATGTCTCTCTGGAAGTGGCAAGGCGGCTGTCCCTTCGACCGAAATTCAAAGTCAGCTGCC  
 TGGTGTTGTAGTGGGAGCTCTACACTGGAAACATCAGACATCTCAAGGAGATGACCGGCGCTCTCGCGAGC  
 CAAGCCCTTCGGCCCGCCAGAGCGAGAGTCCCTCACTGGCTGCAACAGCCAGCTTTGTGGCTCAGCAGTAC  
 ATTCTCTGAGAGCTGGGACGCTTGAAGAGCGATGATGAGGAGATCTACTTTTCTCAGCAGACATGGCAGCTAA  
 TTGTGATCTTTTGAGAACACCATTTGTGCGGACTGTCCCAATGTCTGAAGGCGGATCAGGGTGGAGAGCGGGT  
 CTACAGCAGCGCTGGAACTCTCTCTCAAGGCGCAGCTGTGCTGTGCTCAGGCGCGAGCTGGCTCTCCCTTCAAC  
 GTGCTCAGGATGTCTTTCAGCTGAGCCCGAGCCCGAGACTGGCGTGACACCTTTTATAGCTCTTCACT  
 TCCGACTGGCACAGGGGAATCAGGAGGCTCTGCCGTGTGTCTTCAAAATGAAGATGTGAGAGCTCTC  
 AGCGGCTCTACAGAGGAGGTGAACGCTGAGACACAGCTGTGTACACGTTGACCCACCGGGTGGCCACACCCGG  
 CTGTGAGCTGCTCATCCACAGCTGCCGCGGAGGAAGAGAACTCAACTCATCTCTCAGCTCCGACGACCGGTGCTG  
 AACTTCTCAAGAACACTTCTGATGAGCAGGGCAGTCGGAAGCGCATGTGCTGTGACGCGCCAGCTGCTGC  
 TACACCGGCTCGAGGCTGTACACCGGCTCTGCTGGCTCGGATACACATCATGATGTCTCTCTCGGACGCTGTG  
 GCGCCGCTCCACAGGAGCTGAGGCTGGGCGCCGGTGACACATTTGAGGAGCTCAGCATCTTCTCATGGGA  
 CAGCCGCTCGGAATCTGCTCTGACACCCACAGGGGGCTGTGATCGGCGCTCAGCTCAGCCGCGTAGTCTCAG  
 GTGCCATCGGCAATCTCAGCTGTACCGAGTGTGGGAGCTGCCCTCTCGCCGGACCGCCACTGTGCTGTG  
 AGCGGCTCAGCTCGAAGCACTGCACTCTACCCAGCTCAGCTGGCCACAGGCGGTGGATCGAGGACTCGAG  
 GGAGCGAGCGCCAGGAACTTTGACAGCGGTCTTGCTTTGTGCCCTTTTGTACCAAGCGGGAGAAGCA  
 TGTGAGCAGATCCAGTTCTCAGCGCCAAACAGTAGTGAACACTTTGGCTCGCCCGCTCTCTTCAACACTGGGACCCGA  
 CTCTGCTGACGACAGCGGGGCCCTGAATGCTCTGGCTCTCGACACGCTACCCACTGGGAACTCTGTGCTGT  
 GTGGGACCCCAACAGCTGGGGAGTTTCAGTGTGTGCTGTGCTCAGTAGAGAGGGGCTTCAGCAGCTGTGAGGAGCT  
 TGCCAGAGGTGGTGGAGACGGGGTGGCAGACACCAAGATGAGGTTGGAGTGTACCGCTCATTTACGACATC  
 TCGGTTGTGAGTGCAACAGCTGTGGTGACAGAGGCTCGGGTGCAGACAGAGCTCTTGAAGAGGATCTCTGTG  
 ATGTGACAGCTCTTTGTGCTGGCCTGTCTGCTCCAGTTTATTCTTGTCTACCGGACCCGGAACAGCATGAA  
 GTCTTCTGACGAGGAGGGGAATCTGCGACGCTCGCCACCCAGAGCTGCCCTGGTGTGCCCTCGCCCTCGAGCCCG  
 CCATCTCAAGGCGCTAGGGCCGCTAGACACGCGCTCGATACCGAGGGTTACAGTCCCTGTGACAGCACCCCGC  
 GGGGCGCGAGTCTCTACTGATCAGAGGAGAGGCCATCAGCTACCAAGAGCTCTGTGGAGAGGTTATCCCAAGT  
 TGTCCCCGGCGCGGCTCGGCTGGCTCGGAGATCCGTGAGCTCTGGT**CTGA**GAGCTCTCCAGAGAGCTG  
 TCGCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCACTGGACCTCCCTCCGCTCTGCTCTGTGTGGTGAAC  
 ACGAGCGGTGGTCCGGCCCTTGGAGCCTTGAGACGCTGGCTGTGCTCTCAGTACAGTACGGAAGCTCC  
 TACCACCCGACAGCCCAACAGCGCTGGCCCGAGAGTCTTGCCCAAAATAGGGGGCTGCTAGTGTGTGTGAA  
 CAGTGTCTCTTATGTAACCTGAGCCCTTTGTTTAAAAAACATTCAAATGTGAAACTAGAACTGAGGAGGAGAG  
 ATGACATGGCATCGACACACAGCGGCTGCTCCAGTTCTATGGCTCCAGGGGTGCTGGGATGCATCTCAAATGT  
 TTGCTGAGCAGAGTTGGAACACTCTACCAACTGGCTCTTCACTTCCCAATCTTACCGGTGACCCCGAGCTG  
 CTTGCTGCTGCTGAGATTTCAGAACAGCTTGGGCTGGCTGGCTTGGCTTGGCACTGACGCGAGGATGTAGTGT  
 TGTGTCGCTGTGCTCCACACTCTCAGGACAGAGGGCTAGGTTGCTGCTGCGGCTCACCAGTCTCTGGCTGT  
 GGAACCAACTCTTGCAAGCTTTTCAGCTGTATCAGGCTGTGGCCACACGAGGAGACGCGGAGCTCAGGAGA  
 TTTGTGTCAGATTTACGCTTTTCTCTCAGAAATCAGGAGAGAGCTGTGCTCTGCTTGTGCTGTGAG  
 GAACCGCTGTGCCCTTCCCACATATCCACCTCGCTCATCTTTTGAACCTCAACACGAGGAATCACTAATGCC  
 CTGTGCTCTCCGAGTCCGAGTCTACCCCTCATCTCTCTCTCTCTCAGTCTAAGGAGATCTCAACACTGCC  
 AGCACAGGGGCTGTAATTTATGTGTTTATATACATTTTAAATAGATGCATTTATGTCACTTTTAAATAAA  
 CTCTGAAGAATCACTGTTTAAAAAATAAA

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
```

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFRLR  
EAEHISNYTALLSRDGRTRYLVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQCCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCF  
FDPNFKSTALVVDGELYTGTVSSFQGNDDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFESETGGEFEFFENTIVSRITARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFITLSPSPQDWRDITLYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETTQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPOARYQRVAVHRVPLGHHTYDVLFLGTGDGRHLKAVSVGPRVHIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSSGSCKHVSLYQP  
QLATRPWIQDIEGASAKDLCSSASSVSPSFVPTGEKPCEQVQFPQNTVNTLACPLLSNLAR  
LWLNRNAPVNASASCHVLPTGDLVLVGTQGLGEFQCWSLEEGFQQLVASYCEPVEDGADQ  
TDEGGSVPVIISTRSVAPAGGKASGADRSYWEFLVMCTFLVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPPVLPETRLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIDSFVEVSPVCPRPVRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

## FIGURE 143A

CTAAGCCGGAGGATGTCAGACTGCGGCGCGCGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTCGGAACCGGA  
 CCGGACCGCAGCCGAGAGCCGCGGAGCGGGAGCGGAGCCGCGACTCTGCTTGGCGGCGCTCGTCCGCGCTCG  
 TGGCGGCGCCGCTGCTCCCGCGCGGAGCGGAGGAGCGCGCGCCACCTCGCGCGCCGAGCCGCGCTGCGCGCGC  
 CGGCGACTGGTCCCTCTCTTAAGGCGCAGGCGCGCGCGCGCGGCGGCTGTGCGGAACTAAGCGCGCGCGCGGCG  
 CTTGCGGCGCGCTGCGGCGCGCGGATGGCGCGCGCGCGCGCGCGCGCGCGCTGCCGGGCGCGCGCGCTCG  
 CGGCGCTAGGCGCGGCTGGCTTCGTGGCGGGGCGAGCGGCGTGAGGCGCGCGGAGCGCTGCGCGCGGCGCGCG  
 GCGGCGCGCGCGCGCGCGCGGCGGAGCGGCGCGCGCGCGGCGATGCGCGCGCGCGCGCGCTGCTCAGGCTGCG  
 TGCTCGGCGCTGCTCGGGCTTCGTGCTGGCTCGGCGCTGCTCCTGCCCGGCGCTCCGAGCTGAAGCGAGCGG  
 GCGCCACGCGCGCGCGCGCGCGCGGCTGCGGCTCGGCGCGCGCGCGCTTCCAGCGCGCGCGCGCGCGCG  
 GCGATGCGCGCGGCGCGCGCTCTGGCGCGCGCGCTCGGACCCAGATGGCGCGCGCGCGCGACAGGAATTTCTCT  
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGCGCGTGGCGCGCTACAGAACTGGTCCAGACAA  
 TTCTCTGGGAAAGTTCAGTTCTCTCAAGTAGGGTTCTGCACACTCTGTACCAATTCAGTAGTGCCACTACGGG  
 GTGTGGACGACTCTACCGCGCCCGAGAAGTCTCTCATGATGCTCAAGTACATGCACGCCACTACTTGGACA  
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGGAGACCGCTCTGGAGAACTTCTGAGGAGTT  
 TGAACAGCAGCGAGCCCTCTTCTTGGGCAGACAGGCTTGGGCACCGAGAAAGTGGGAAACTGGCCCTGG  
 AGCCTGGTGAGAACTTCTGATGGGGGGCGCTGGCGTGTATGAGCGCGGAGGTGCTTCGGAGAACTGGTCCCGC  
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCTTGAAGACTGGAGTGGGAGGTGTGTCCGAGGTTGT  
 CAGGGGTGCAGTGTCTGCTGCTTATGAGATGCGGCGAGCTTTTATGAGAATTACGAGCAGAAACAAAGGGGT  
 ACATTAGAGATCTCCATAAGCTAAATTCACCAAGCTATACATTACACCCAAACAAACCCACCTTACAGT  
 ACAGGCTCCACAGCTACATGCTGAGCGCGAAGATATCCGAGTTCGCCATCGCAACATACAGCTGACCGCGAA  
 TTGCTCTGATGAGCAATACGCAACACAGAAATTCATAAAGAGGACTCCAGCTGGGAATTCCTCCCTCTTCA  
 TGAGGTTTCAGCGCCCGCGAGCGAGAGGATCTGGAATGGGAGTTTCTGACTGGAAATCTTGTATTCGGCAG  
 TTGACGGCGCCCGCTCGAAGCGAAGATGGACTCCGCGAGAGGAGGCTTGGACAGCACTTGTATGAGCTCA  
 TGAGAGTATGATCAATGCGCCAGCCAGACGAGGGCGCATCTGACTTCAAGAGACTTCAGTCCGCTACCGCC  
 GGGTGAGACCCCATGTATGGGCTGAGTACATCTGGACCTGCTGCTCTGTACAAAGACCAAGGAGGAAAGAA  
 TTGACGCTCCCTGTGAGGAGGACCGCGTATTTACGACGACTTTTCAGCAAAATCCAGTTTGTGAGGACTGAGGAG  
 TGGATGCACAGAGTTGGCCAGAGATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACTCCCTGAAGA  
 AGCTCTGCTCCCTTTACGCTCCCTCGAGGTGGAAGAGTGAGCACAAGAAACCAAGTAAAGATTAACATACTGA  
 TCTCTTTGTCTGGGCGTTTCAGCATGTTTGTGAGATTTATGGGAAACTTTGAGAGAGGTGTCTTTATCCCAATC  
 AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACTGACAAAGCCCAACAGTTGACTGATGA  
 GAGATTACCGCATTAAGTACCTTAAAGCGGACATGCAGATTTTGGCTGTGTCTGGAGAGTTTTCAGAGCCCTGG  
 CCCTGGAAGTAGGATCTCCCGATTAAACATGAATCTTTGCTCTTCTTTCGCGAGCTCGACCTCGTGTCTTCTA  
 CAGAATTCCTTCAGCGATGTCGAGCAATACAGTTCTGGGCCAACAATATATTTTCCAATCATCTTCAGCCAGT  
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAAACATTTTGCCTTTACTCAGAAAACTGGCTCT  
 GGAAGAACTATGGGTTTGGCATCACTGTATTATAGGGAGATCTGTCCGAGTGGTGCTTTGATGTTTCA  
 TCCAAGCTGGGGCTGGAGATGTGGACCTTTCAACAAGGTGTCCAGGCGAGTTTGAAGAGCTTTAGGAGCC  
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTCTGCTTTTGTATCCCAATCTTGACCCCAACAGTACAAAATGT  
 GCTTGGGTCCTCAAGCATGCAGATTTGGGTCACCCGACGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
 GTTACAGTAAAAGCAGCAATAATATGGCTCAGTGAGGACAGCTTAAATGTCCAGCTTTGCTGGAAAAAGCGTTTT  
 TAAATATCTAATTTTTCATTAATTTTTCATTAATTTTGAAGTGCATTTTGAAGTGCATATACAGGATATATTTAC  
 AAGTGGTTTCTTCAATAGGACTCCTTAAAGTTGAGCTTCTGAACAGAGAGTGATCAGTGTTCGCTTTGAA  
 CACATCTCTGCTGAACATTATAGCAGACCTGCTTAACCTTGACTTGAATGTACCTGATGAACAAACCTTT  
 TTTAAAAATGTTTCTTTTGAAGCCCTTGTCTCCAGTCTTATGGCAGAAAGCTGAACATTCCTGCAAGATAT  
 TATTGTCAAAAGACTGTAACCTGTGTAATGTCTGTGATTGTTAACTTCCAGAGTTCCAGATTTCACTTTGT  
 GTTTTGTTTTTTTTCATATTGTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
 GCTGTTTCATCATGTTGCTTCAGGAGGCTTCCAGAGTTGATCATTTCTCATGGTACTCTGCTCAGCATGGC  
 CAGTAGGTTTGTGTTGTTTGTGTTGTTTGTGTTTGTGAGACGAGCTTCATCTGTATCCACGAGCTGGAAT  
 CAAGCCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGTTCAAGCAATTCCTCGCTTTCGCTCCGCGAGT  
 AGCTGGGATTACAGGACACACACCCAGCCAGTATGTTTGTGATTTTTGTAGTAGAGAGGGGTTCACCAT  
 CGAAGCCGAGCTGCCACGCTAGGTTTAAAGCAGGCGGCTGAAGAGGCAGCTGAGGATGTGGGTGTTCTGCG  
 TGGTAGTCTTCGCGCTAAATAGACCTGGCATTAATTTCAAGAGAGGATTTGGCAATTTCTCTCTTCAACCTG  
 CTCTTTAAAGGCTAAATATTTAGTGTAGAAAGCAAGATGAATTAACATAAATCTGATGACAGCACT  
 GAACATACACACATACACCTTAATCAAACGCTGGGGAAAAATGTATTTGGTTTGTCTTTCATCTGCTGCTG  
 TGTATGTGGGTGAGATGTTTTCATCTCTTCACTACTGTTTGTATTCCTGTTATCTGTAATACCTTTAA  
 TTTATTTAATATCTGTTTTCAGAGCTCGCAATTTCTGAGTACTGTTAGTTAGTATTTATGATGTCGG  
 GAGTGTGTTTGTGTTTATTTTCAGTAAACCGATCTCAAGAGATTTCTTTTGGAAACGCTTTTCCCTCC

**FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAAATACACGTCATTGGAGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTIGGAAAATAAACCAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGCTCATT  
ATTCTGTTTGTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAAATTAACACGAAAAA

10020053.121301

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
 GDARGAQLWPPGSDPDGPPDRNFLVFGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
 SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLNENFLR  
 SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
 THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKGYIRDLHNSKIHQAITLHPNKNPP  
 YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE  
 ILEWEFLTGKYL SAVDGGPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
 GYRRVNPMYGAEYILDLLLLYKKHKKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
 INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
 LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
 FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPDNDHFAFT  
 QKTGFWRNYGFGITCIYKGDVLRVGGFDVSIQGWGLEDVDLNFNVVQAGLKTFRSQEVGVVH  
 VVHPVFCDPNLDPKQYKMLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

1002003.12334

GGACAACCGTGTGCTGGGTGTCCAGGGCGCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGGACGACGCCAT**TATGA**AGCCCTTAGTCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCTCTGGGAGCCAGGTCGTGAGAAAAATC  
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACGCGAAAGTACCCC  
ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAATGAAGAGCCAGAGCCGAGAGCCGGAGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCTCAGCTCT  
CAGGTGAAACTGCGATAGAAAAACCCGAAGGTTTGGAAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAaaaaaaATTTTAGATATTAATTCAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAGATCACCTAAAAACGAAGC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAaaaCAATGTATAAGTCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAACTGCTGTGTAATTC  
TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACAGAGATGAGAGAAAAAG  
CTGCTACAGTATTTCAATACATTAaaaaATATGTGTAGTACAAGGAGTACAGCGCTTATTA  
AAAGTTTAT**TAA**ACCATATATAAAAAATTTTAAACTACTTGATATTCCATAACAAAGCTGA  
TTTAAGCAAACGATTTTTCACAGAGGAAATAATCATATTGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGTTTCAGGAAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

1002003-121301



**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAATATCCATCCACCCCTGCTGTATCTGTTTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATGG**CCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCTCTTTCTCTGAGACCACTGCAGAGGCTATGGAAGTGC GGTTCTCTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGTGTGCTGAGTCCAGTATCCAGATTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCACAG  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCAATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGGAAAATCCA  
 GGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACAG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGATTTTCA  
 ATTCATATCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTATACC  
 CTGCTGACATGTGAGTTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTATATATGTCAGTGTCTTGGGGAT**TC**GACAGAGAGAAGCCCTG  
 CTTAAAGGGCCCCACACCACAGACCAGACACAGCCAAAGGGAGAGTGTCTCCGACAGGTGGC  
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCAAGCCCCCACTCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTGTGTTGTGAAAACCTCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGTGATGACTCAGGACAGTGATTCCTGCCCTCACAGGTGAAGATTAAGAGA  
 CAACGAATGTGAATCACTGCTTGACGTTTGAAGGCACAGTGTGTTGCTAATGATGTGTTTGA  
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTATTCCACATTAATTTACTTTTCTCTA  
 TACCAATACCCATGGAATAGTTATTAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
 GAGGTAGGATTTTCTAGTGATCTATAAGCCACGACATTACCTGATACCAAAACACAGGCAAG  
 AAAACAGAAGAAGAGGAAGGAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTTTAAACAAATTAACATAACAAATATATTAAAGATGATATATACTACT  
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATTTAAATATCAACAGTGTAAAT  
 CAGCACATTAATAAAGTAAAAAAGAAAAACATAAAAAAAAAAAAAA

1020063.121301

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPPSPWRLASILLGLLCGALC  
GVVMGMIIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDGRKNNVTLS  
PNNGYWVLRRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

1002005-121304

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAA  
 TTACTATAGCACATTGTCAATTTACAACAGCAAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCCTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCATAAGTA  
 GATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGATCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAAATATAA  
 GAACCTTGCCAGATGGACTGCTTCCCTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTACTCTGGAGGACCACCTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAAACAG  
 CCTGGTGTTTATACTAGAGTTACGCGCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**  
**AGAGACAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT**  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGGCTTGATGCATGATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTTCATTTGTTCTCTAGAAGTTTGTGAGAATTTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTCAGTTCCCTC  
 AGCTCCTCTCATTTACAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCTCATATTTTATTTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAGACAGCAGAAATACCAATC  
 ACTTCATCATTTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG  
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAATCACCCA

**FIGURE 150**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTINYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDASYEQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

```

**Transmembrane domain:**

amino acids 21-40 (type II)

10020003.121301

**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTTCTCCCCGGTCCCTCCACTACTGG  
 CTGTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAACCTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTTCGTAGTGGCCGCTA  
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
 CCTGCCTTCGGGCCCTTGACCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC  
 GGCCGTTCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCGAGGGGCGCTCTGA  
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
 GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTA  
 AGCGGCCAGATAATAAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

1020063.121301

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874  
><subunit 1 of 1, 238 aa, 1 stop  
><MW: 25262, pI: 6.44, NX(S/T): 1  
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHRHLQVPCKE  
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAFFSPVLHYWLLLDWGSEA  
AQKGPPPLNATVRRAEKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRRAARAAGAL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG  
 CCCAGCGCCGACGATCGCTGCCGTTTGGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACA**ATG**CCAGAGAAGATTCCGTGAAGTGTCTGCCCTGCTTGTCT  
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAACGAGTC  
 ATTTTGACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCCTGTTTCCCTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAGAACTGTGCTCTTCTGCATGGTACT  
 TTGGAAGTTTGGTTGTCATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACCTATGGTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCAGAT  
 TCCTGCTGTGTAGAGAATTTCCAGGATGTTCCAAACAGGCGCCACAGGAAGATCTCAGTGA  
 CCTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTCAGAGGAACCAACAACTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTAT**TAA**AAAGAAATGTACAGAGAAGAAACCAAACTGTTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAAAGTTTCTATGCTAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCCTGTTGAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTC  
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAACTATAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTGTGCTTACTAAAAATATTCTTACCACTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAAATTCAGTCGATTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTTGTCTGTATAGCATCATTATTTTAGCCTTTCTGTTAATAAAGCTTTTACTATTCTGT  
 CCTGGGCTTATATACCATATAACTGTTATTTAAATACTTAACCACTAATTTTGAATAATA  
 CCAGTGTGATACATAGCAATCATTATTACAGAAATGATGCTGGCTTTAGGAAGTATTATAAA  
 GAAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCCAATG  
 AAGACTCTTTTTCACATAAACACATTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAGAA  
 GCAATAGTCTCCAGTCAATATAAATCTACAGAAAAATAGTGTCTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAAAACATGTGACAAATTTAGAGATCTTTGTTTTATTTCAGTGATTA  
 ATATACTGTGGCAAATTACACAGATTATTAATTTTTTACAAGAGTATAGTATATTATTT  
 GAAATGGGAAAAAGTGCATTTTCTGATTTTGTGATTTTGTGTTTTTCTCAGAAATATGGAA  
 AGAAAAATTAATGTTGCAATAAATATTTTCTAGAGAGTAA

10020063.121301

**FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQ
WSDMVTCLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
 TGCACCTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATGT**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGTCTCTCATCAAGG  
 TGATCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCAGAGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAAGTGGTCTCTGCGCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACAGGATCTGGA  
 TGTGTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT  
 TCTCAGGCTCCCTGGTCTCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCGT  
 GTGGTGGGTGGGAGGAGGCCCTCTGTGATTCTTGCCCTTGGCAGTGCAGCATCCAGTACGA  
 CAAACAGCAGCTGTGTGGAGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT  
 GCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
 AGCTTCCCCTCCCTGGCTGTGGCCAAGATCATCATCATGAATTCAACCCCATGTACCCCAA  
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTACTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGTGTCAGGCGTCAGTCCA  
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGGCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
 GGGCCCGAGCACCCAGAGGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCACTGCTGGGAGCCGCTTCTTCTCTG  
 CCTGCCCACTTGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGGTACACCC  
 CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCTCTGTAAGAGACC  
 TCGCAGCCACAGAGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCC  
 AGCATCCCAGGGAGAGACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAAAA

10020067.121301

[illegible]

## 10



**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGACGCGGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCAGCCCTGGGCTCGAGCCCTGGAGCCTCTCGGGCC  
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCAGCAGCAGCCGCGGGGGAGGCGGGCAGGGGCCCATGCCA  
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTCTTCCACCAGGAAGGCCCTCCAGGATTTTGACA  
 CTCTGCTCCTGAGTGGTGATGAAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG  
 ATCCAGGGGTCCCAGGCTAAAGAACATGATACCTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
 AGAAGAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTCAACCATCTCTACA  
 CCTCGGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG  
 AGGACAAGGTCATGGAGGGAAAAGGCCAAGCCCTTTGACCCGCTCACAAGATACGCTGTCTTGGTGATG  
 GGATGCTCTATTCTGGTACTATGAACAACTCTCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGC  
 CTGTCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCTCTCTTTGGGACGCCATCCCTTCGACCC  
 AGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGCGGGCAAAAAGCTGCTCAGAGAAGTGGACCACTCTCTGAAGGCCGAGC  
 TGCTCTGCACCCGCGCGGGAGCTGCCCTTCAACGTCATCCGCCACGCGTCTCTCTCCCCGCCGATTCTCCCA  
 CAGCTCCCCACATCTACGCACTCTTCACTCCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCT  
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAGAACTTACAGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCACTTGCTCAGTGGGCCCCCTCTCTGATAGGCCCTGACCT  
 TCAAGAAGGACATTCTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGCGCTGGAACTATA  
 CACGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCCACAG  
 GGTGCTCCACAAGGCTGTGTAAAGTGGGACAGCAGTGCTCATCTGGTGGAAAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCAGGTTGCACTGTTTGTAGGCTCTCAGGAGGTGTCTGGA  
 GGGTCCCCGAGCCAAGCTGTAGTGCTATGAGAGCTGTGTGAGCTGTCTTGGCACTGTCTTGGCCGGGACCCCACTGTCCT  
 GGGACCTGAGTCCCGAACCTGTTGCCTCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGGCTATGTCCAGTGGCCCATGAGCAGGAGCCTTCGGCTCAGAGCCGCCGCAATCATTA  
 AAGAAGTCTGGCTGTCCCCAACTCCATCTCGAGCTCCCTGCCCCACCTGTGAGCCTTGGCTCTTATTATT  
 GGAGTCATGGCCAGCAGCAGTCCCAAGGCTCTTCCACTGTCTACAATGGCTCCTCTTCTGTATAGTGCAGG  
 ATGAGTGGGGTCTCTACCAAGCTGTGGCAACTGAGAATGGCTTTTCATACCTGTGATCTCTACTGGGTGG  
 ACAGCCAGGACAGACCTTGGCCCTGGATCCTGAACTGGCAGGATCCCCCGGAGCATGGAAGTCCCGTTGA  
 CCAGGTCAGTGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTCACTGTCACTGTCTCT  
 TTGCCTTAGTGCTTTCAGGAGCCCTCATCTCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGG  
 TTCAGGCTGTGAGACCTCGCCCTGGGGGAGAAGGCCCGTGAAGCAGAGCAACACTCCAGTCTCCCAAGG  
 AATGCAGGACCTTGCAGTGTGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGGTGGGTGCAGGCACTGGCCATGCTGGCTGGGCGGCCAAGCACAGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
 ATGCACAGCACTGTGCCTCCCTATGGGACTCCCTCTACCAAGCAGATGAGCTCTCTAACAGGGTGGGGCTAC  
 CCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGATCTTCAAGTCTGGCCATTCCAGGGACCCCT  
 CAGAAACACAGTGTTCAGAGACCCATAAAAACTGCTGTGCCAGGACCCATGGTAATGAACACCAACATC  
 TAAACAATCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  
 TCTCCAGGGTCATGAGGGATCTGCTCCCTCTGCTTCCCTTACCAGTCTGTCAGCCGCTGACTCCGGAAGTC  
 TTTCTGAAGTCTGACCACCTTTCTTCTTGTCTCAGTTGGGCGAGCTCTGATCCCTCTGCGCTTGGCAGAGTGG  
 CAGGGGTAACTCTGAGCCCTTCTCACTCCTTTACCTTAGCTGACCCCTTCACTCTCCCCCTCCCTTTCTCTTTGT  
 TTTGGGATTAGAAAACCTGTTGTGAGAGCTGTTATTTTTTATTAAAAATATAAGGCTTAAAAAAA

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
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><subunit 1 of 1, 761 aa, 1 stop
```

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPFWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYIYAGDERRALSFFHQKGLQ  
DFDTLLLSGDGNTLYVYGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTA  
VLVDGMLYSGTMMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASVFAAIPSTQVVYFFFE  
ETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN  
CSVYESCVDCVLARDPHCAWDPEsrTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLP  
QSRPQI I KEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLILYQDVGVG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVLPTRVSGGAALAAQQSYWP  
HFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVEDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATGG**CTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCGCTC  
 TCAGAGGCTGCCAAAATCTTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAACTTATTAATGTTCTAGAATACTTGGGCTTGCAAGTCAGCTC  
 ATTTTAAATAGAAAAGGATATCATGGATTCTTAAAGAATGAGAATTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC  
 CATTCTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCCCTGTCTTATGTT  
 CAGTATTCGGTTCTTGTCTGACTGATCAGATGGACTTCTGGGGCCGAGTGAAGAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACCTGACTTTGCTTTGATTGTGCTGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGA AAAACCTATTAACCAGTACCACAAGACTTGGAGAATCTTATTGC  
 CAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCA  
 ATCCGGAATCTTCAAGGAGATGAACAATGCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCAGTGTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAATGTGAAAATTGTGGA  
 CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGCTGTGTTGTGCCACCGGGC  
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTATTCAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGAGTGCTGTCAGTGTCTGCTGCCCTCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGGACGACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGACGTTTTTGTGTTTTGCTGGGGC  
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCT  
 GGGGCCAGAAAGGTGAAGGAGACATA**AGG**CCAGGTGAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTTGGCAGCCCCATTCTCTAGTCTCTC  
 TAGTTATCTCTGTTTTCTGAAGAACAGGAAAAATGGCCAAAATCATCTTTCCACTTGC  
 TAAATTTTGCTACAAATCATCTTACTAGCTCCTGCTGCTAGCAGAAATCTTCCAGTCTC  
 CTTGTCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCCTCAGATTTCCAGCCTTAAATCCACCTTCTTCTCATGCGCTCTCCGAA  
 TCACACCCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCTCTGCCC  
 TACTATCTATCATGGAATAACATCCAGAAAGACACCTTGATATCTTTTCAGTTTCTGTTT  
 TGTTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCCGTGCTCTGAGAGTTTCAGGGC  
 CGGACACAGGCTCAGAGTCTCCACATTTGGGTCCTGTCTCTGGTGCCACAGTGAGCTCTCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAGTTTACA  
 GCGTTATCTCTCCCAACCTCACTAA

10020053.121301

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169  
><subunit 1 of 1, 523 aa, 1 stop  
><MW: 59581, pI: 8.68, NX(S/T): 1  
MAGQRVLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHNKRGPFMPDFKKEEKSYQVISWLAPEHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGTLWL CGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

10020003.121301

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTTCTGTCACACCCGTCACACACATACCATGTT  
 CTCCATCCCCCAGGTCACAGCCCTCAGTGCTGTCCATCCAGCAGGGCTACCCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGGTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCCTAGAGAGGGC  
 AGACTATCAGGGGTGCCGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCAGA  
 AGACCGGGGCACTTGTGGGTGTCAGAGCCCTCAGCCATGTTGGGAGCCCAAGCCACTGGC  
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCCACCCCTGGGC  
 GAGTGGCATTGTCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACCAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTATCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAAGCTGTGTCTACTGCCCTTGGG  
 CCTGGGGACCGAGTGCTCTGCGCCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAATACT  
 CAAGTTTCTCTGGCTTCTCTATCTTCCCTCTCTGAGGAGCCCAAGTCTTTCAAGCACAAGAAT  
 CCAGCCCTTGACAACCTTTCTTCTGCGCTCTCTTGGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGTCATGGGACCCCTGTGCCAAACACCCAAGTTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
 AGAAGGAAGATCTGCATACTTTGCGGCCCTGCTGCTCCTCCGGTTCCCCACCCAGCTTCTCT  
 GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGACAGCCGCCACAGGAGGCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC  
 TCAGCCAGCACCCTCAGAAGCTGAGCCAGCACCCTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGCAGAAGGTTGGGAAGGGCTTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACTGAGATTAG  
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAACAATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCCCAAGCTCTC  
 TCACTGAGTTATCTTCACTGATACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCTGAT  
 CTGTGCTGTCTTATTTCTCTCTTAGGCTTCTATTACCTGGGATTCCATGATTCATTCTCT  
 CAGACCTCTCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT  
 GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTTCAGTGAGACATAT  
 AGAATTACTAAGGAGAAGATGCCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGTA  
 TGTTCAGAGGAAATAAATACAACTGTATACATAAAATTAATA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLPLHSPGLPLVLVLLALGAGWAQEGSEFVLLEGECLVVCEPGRAAAGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGLIFPL

**Signal peptide:**

amino acids 1-32

1022053.121301



[illegible]

**FIGURE 164**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVIVSVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRVWQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIITPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

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**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGCGCCGCGGATGGGGCCGGGGCGGGCGGCCGCCATCTCGTAGAGGCCGACGAGGCGGGCCGGGGCCCA  
GGGCCGAGGAGCGCGCGGCCAGAGCGGGGCCGCGGGAGGCGAGCGGGGACGCCGCGCGCAGCAGCAGGTGGCG  
CGGGCTGCAGCGCTTGTCCAGCCGGAGGCCCTGAGGGCAGCTGTTCCCACTGGCTGTCTGACCTTCTGCTTGGG  
CGGGCTGCTCCAGCAGGGGGCCCTGCCACCGCTCTGAGCAGCGCCATGCGCCCTGCTGGCCCTTCTGGAACGACG  
TCTCGTGCTGACCTGCTGGTGCGGCTTGTCTTCCTGGGTGAGTGGTCTGTGTCATCAACTTCGTCCAGCTGTGCAC  
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCTCGCCTACTCACTCTGAGGCCA  
ACTGGTCATGCTGCTGGAGTGGTGGTCTCGACGGAGTGTACACTGTTACGGACCAGGCCAGGTAGAGCGGCTT  
TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTTCAGATCGACTTCCTCTGTTGGGTGGACCATGTGTG  
CGCCTTCGGAGTGTGGGAGGCTCCAGGTCTCGGTGAAGAGAGCTGCTCTACGTGCCCTCATCGGTGGTGC  
GGTGAATTTCTGAGATGTTGTCTCTCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCAAGGGCTGAG  
GCGCCTGTGCGACTACCCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA  
CCGCGTTAGCATGAGAGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGTCGCGGGACCAAGG  
CTTCAACCCAGCAGCTCAAGTGCTCCGGGGACAGTCAGCACTGCTATGATGTAACTGAACTCAGAGGAAA  
CAGAAGACCGCTCGCTGCTGGGATGCTCTACGGGAAGAAGTACGAGCGGCATGTGTGCTGAGGAGATTCTCT  
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACAGGAGAAGGACGCGCTCCA  
GGAGATATATAATCAGAAGGGCATGTTTCAGGGGAGCAGTTTAAGCCTGCCCGAGGCCGTGGACCTCTCTGAA  
CTTCCTGTCTCTGGGCCACCATCTCTCTGTCTCCCTCTTCAGTTTGTCTGGCGCTCTTGGCCAGCGGATCAC  
TCTCTGTGACTGTTCTTGGGTTTGGGAGCAGCTTCTTGGAGTTCCGAGACTGATAGGAGATACGCT  
TGAACCTGGGAGGTGGAGATGTCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCAGAAATTCGGAGTTGAATGTGTAGTTACTGACATGAAAA  
ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGCGAGAAAAAATCAGCAAGCTTGAAGATGTGACTTGTAGATT  
TTTCAGGCTAATGAAAAAAGATGAAGGAAAAATTAACAGGCTCAGAGACCCATGGTGACCTGCACACAAATCAA  
CATATCGCATGATGAGAGTCCGAGAGGAGGAGGAGCAAGGGTCAGAAAGAAATGGCCACAGCTGATGAAAAACA  
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA  
AATCAAAGTGTCAAAATGACAAAGATCTGGAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATCTTTG  
ATCAGATTAAACAGCTCATTTTCTCTCAGAAATCATGGGAGCCAGGAGATGTGGGATGAACACTTGAAGGACA  
AACCTTCACTGTAAATTATTGGACATTTTGAAGCTCTAGATGGTCTGACTCTTTGGTCTCAGGAGCAATTTTCA  
ATTTAATCCCTAATAACAAATAGTCAAGCTTCTTGTGACTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGG  
TTACACCTGTAATCCAGCAGCTTTGGGAGGCCAGAGCGGGATCATTGGGGTCCAGGCTGATCTCAAATCCT  
GAGTTCAAGTGATCTGCGCGCTCGAGCTCCCAAAGTGTGTTGGTTCAGCGGCTGAGCCGCTGCGCCTGGCCGA  
ATTTCTTTAAAGCTGAATGATGGGCTCCAGGACAGCATGTGCTCAGCCCTGTGATCCCAAGTAGTGGATTGTA  
AACAATGACCAACCATCTCGCTGCTAATTTTGTATTTTGTAGTAGAGAGCTGTTAGCAGGCTGTGTCGATCTCCT  
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCCTTGA  
GCATCTTGTGATGTGCTATTGTGGCATTGTATATCTCTATCTCTTTGGGGAATGTCTGTTCAAGTCTCTTTG  
CCTTTTTAAATTTTTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT  
CAGTGGCACAGCTCTGGCTCTGCTCAGCCTCGACCTCTGGTGCTGAGTGAATCTCCACCTCAGCCTCCCTGT  
AGCTGTATTTTCTGTATTGTATTGTTAGTGTAGTGTGTTGTTGTTATTTTGTGGAGCAGCATTTCACCATGA  
TGCCAGGCTGGTCTTGAATCCTGAGCTCAAGTGATCTGCCCTGCTTCAGCCTCCCAAAGTGTGGGATTCAGCA  
CATGAGCCACTGCACCTGGCAAACTCCCAAATTAACACACACACACAAAAAACCCTGATTCAAATGGGCA  
GAGGGGCGGGGTGGCCCAACTACAGGGAGACTGAAGTGGGAGATCGCTTGGGCATGAGAATGAGAGCTG  
CAGTGATCGAGGTTGTGCGAGTCAGTATCCAGCTCGGACACAGTGAAGACAGTGAAGCCTGTCTC

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
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><subunit 1 of 1, 368 aa, 1 stop
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><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTKQFVLHLLVG FVFVVSGLVIN FVQLCTLALWVPVSKQLYRRNLNCR LAYSLWSQVL  
MLLEWWSSCTECTLTFTDQATVERFVGKEHAVIIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCRKWEEDRDTVVEGLRRLSDYPEYMMWFLLYCEGTRFTETKHR  
VSMEVAAAKRGLPVLKYHLLPRTKGFTTAVKLCRGTVAAVYDVTLNFRGNKNPSLLGILYGKK  
YEADMCVRVFLFDIPLDEKEAAQHLHKLKYEKDALQEIYNQKMGFPEQKPARRPWTLLN  
FLSWATILLSPLFSPLVGVFASGSPLLILTLFLGVGAASFGVRRLIGESLEPGRWRLO

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTGCTTTAGCACTGGGGCACTTCTT  
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
 GCTTACGCCGTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
 TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT  
 ACATGTGGTGTTCTCTTGTCTGTTCTCTG**TAA**TGTGGTATGCCATGGGGTCTTTCACAAGCCT  
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTTCTTCTACTTAATATGTAGTC  
 ATCCTGCGAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
 CTTGTTTAAATGCTCTCATAAGACCCTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCCTGCCAGGTATAGTGCTACATGTGGTGGTGCT  
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
 GATGGTGTAGGGCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
 TGCAGGTCTTGATTTCAGTAGGCCCAGGTTGGGCATCTCTAACAACCTCCACGTGATGCTGA  
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAATTAGCTG  
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
 AGAGTGAGACTCTATGTCCAAAAA

**FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234  
><subunit 1 of 1, 143 aa, 1 stop  
><MW: 15624, pI: 9.58, NX(S/T): 0  
MHHS LQCPGAATRH IHL CVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR  
EGKINFYTN GDSWGLR PASSVKFLGSAYTFFSLTWH TLLKASQGFSLFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:****Signal peptide:**

amino acids 1-28

10020053-121201

GGTGGTACTGGAACCTCTGGTCCCAAGTGATCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCTACCTAC  
ATTAAATCTGTTTTTTGTCTCTGTGAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAAACAGAGTTTCTACCCAC  
ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCAGCTCTGGAGGCACCTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGCAAGCCCCGAAGATT  
CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCAGCTGCCCGCCCAT  
CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACCTCTGTCCCAAG  
AACCACAGAGCTTGAGTGAGCTGTGGCTCAGACCAGAAGGGCTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCCATTCTCTGGAACATAGGGGAAGCCGGAGGAAAGCAAGTGGCA  
GGGAAGGAACCTTGTGCCAAATATGGGTGACAAAGAAATGGAGGTGTTGGGTTATCACAAGGC  
ATCGAGTCTCTCTGCATTCACTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAGTGACCATTCTCTCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCAGGAGGTGACGAGGCCTGAGAGTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAATGCCTCCAGTAAGCAGAGGTGCAAAATCCCAGGCAGCAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTTGAATTTGAAACCCCAA  
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAAGGATTCAGACCAAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCAGGACTGTGGT  
GTGTGCCTGTATCCAGCACTCGGGAGGCTGAGACAGGAGAAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAACTCACTTCACTGAGCAACACGAGAGACTCTGTCTCAGA  
AAAAATAAAAAAGAATTATGGTTATTTGTAA

**FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA  
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

10020063.121301



**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCTGCTTCCCCCGAGGACAGCCGCCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGACCTTCACGGGCTACTCCGCC  
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
 GCCCCGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGGAGACCTGGACGAGCTGCTGGCGCGGGCGAGGCCGGCACCTTC  
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGTGC  
 AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTGAGGCTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
CTAGGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTAAATTGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

702003.121304  
 10221.902500

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
```

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQVPVRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCCLFFPEDSRLWQYLLSRS  
MREHPALRLRLLTLEQPGQDSMMTCEQAQLLANLARLQAKKALDGTFTFGYSALALALAL  
PADGRVVTCEDVACQPELGRPLWRQAEAEHKIDLRKPALETDELALAAEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQFPKGDVAAECVRNLNERIRRDVRYIS  
LLPLDGLTIAFKI

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
```

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHPWPARIDDADGAVKPPPNKYPIFFFGTHETAFLGPKDLFFPYD  
KCKDKYKGPKNRKGFEGLWEIQNNPHASYAPPVSSSDSEAFANFADGSDADEDDERDRG  
VMAVTAVTATAASDRMESDSDSKSSDNLKRRTPALKMSVSKRARKASSDLQASVSFSE  
EENSESSSESEKTSQDFTPEKKAARAPRGRPLGGRKKKKAFSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSDSDSVYKPPRGRKPAEKPLPKPRGRKPKPERPSSSSSDSDSDEV  
DRISWKRREDEARRRELEARRRREQEELRLRLREQEKEEKERRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPAELEREAKSKAKPQSSSTEPARKPGQKEKVR  
RPEEKQQAQKPVKVERTKRKSEGFSDMRKVEKKKPEVEEKLQKLHSEIKFALKVDSFDVKRC  
LNALEELGTLQVTSQILQKNTDVTVALKKIRYKANKDVMEKAEVYTRLKSRVLGPKIEAV  
QKVNKEAMEKEKAEKLAGELAGEAPKEKAEKDPSTDLSPVNGEATSQKGESAEDEKEHE  
EGRDSEEGPRCGSSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

## FIGURE 175

GTTGGTTCTCTGGGATCTTCACCTTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA  
 ACACCAATTTGAAAGAGAGACATTTGTTTTCATCATGAATGCTAATAAAGATGAAGACATTAAGGCCAGAGGCCAGA  
 TTTTACACCTTTTCTCGCTTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTACTGGCACTTTGAAGCA  
 AAATATTTCCAGAGCTCAGGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGATTTCCCTTTTGGGTTCTATC  
 AGAAGGACCTGGATTTTCAAACCTTCTCTTAGATAGGAAAGAGGCGAGGCTGCTCTTGGGAGCCAAAGACACCAT  
 CTTTCTACTCAGTCTGTTGACTTAAACAAAAATTTAAGAAGATTATTGGGCTGCTGCAAAAGGAACGGGTGGA  
 ATTTATGTAAATTAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTCTCAGCCCTATAACAA  
 AACTCACATATATGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
 GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAATGTCCCTTTCCGATCTTCAGCAGCC  
 TTTTGCTTCAGTATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAGATACTGCAATT  
 CACTCGATCCCTTGGGCCCTACTCATGACCACCCTACATCAGAAGTGAATTTAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATTGGAACCTTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCTCCTTTCTCGAGTTGGAAGAGTTTGTGAAGAATGATGT  
 AGGAGGACACAGCAGCTGTATAAACAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGGAAG  
 TGATGGGGCAGATACTACTTTGATGAGCTCAAGATATTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATGTGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGTGTTTGTGTATAGCATGGTGCACAT  
 CAGAGACTGTTTTAATGGTCCATATGCTCATAGGAAGTGCAGACCATCGTTGGGTGCAATGATGGGAGAAAT  
 TCCCTTATCCAGCGCTGTGATGCTTCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
 TGATGTCATCTGTTTCAATAAGCGGCCTCTGTGATGTATAAGTCGATACCCGATTCGAGGAGGACCAACGTT  
 CAAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCAITTCGAGAAGATGGCCATACGA  
 TGTAATGTTTCTTGAAGACACATTTGGAACCTGTCTCAAGTTGTGACAGATGCGACACTTATGGGAAAGT  
 TGATGCTAGTCTGGAGAGTGTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCA  
 GCAACAACTGTACATTTGGTCCGAGATGGATTAGTTAGTTCAGCTCTCCTTGACAGATGCGACACTTATGGGAAAGC  
 TTTCGCGCACTGTTGCTTCCAGAGACCCCTACTGTGCTGGGATGGAATGAGTACTGCTCGATATGCTCTCTAC  
 TTTCAAAAGGAGAGCTGACGCCAGATGTAATATGCGGACCCAAATCACCAGTGTGGGACATCGAAGACAG  
 CATTAGTCATGAACCTGCTGATGAAGAGTGATTTTGGCATTTGAATTTAACTCAAGCTTTCTGGAATGTATACC  
 TAAATCCCAACAGCACTATTAAATGGTATATGATTGGAATTTGCAGAAAGAAGGATCTGGGATGTATTACTG  
 TGAAGAATCATCAAAAGCGGAATATGGGCTACTGATTGGAATTTGCAGAAAGAAGGATCTGGGATGTATTACTG  
 CAAAGGCCAGGAGCACCTTTTATCCACACCATAGTGAAGCTGACTTTGAATGCTATTGAGAAATGAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAGA  
 CTACATCCAATCCTTAGCAGCCCAAACCTCAGGCTCGACCGTACTGCGCAACAGATGCGCACAGGAGAAAGCG  
 GAGACAGAGAAACAAAGGGGGCCAAAGTGGGAAGCACATGCGAGGAATGAAGAGAAGCAAAATCGAAGACATCA  
 CAGAGACCTGGATGAGTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTAATTTAAGAAGAAAGATTCCTTACC  
 TATAAAAACATTGGCTCTGTTTTGTTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGC  
 CACAAGACAATAATCTGAATAAGACAATATGTATGAATATAAGAAGGGCAAAAAATTCATTGTAAACAGTTT  
 CCAAGAAACAATCTTGCACAAGCAAAGTATAAGAATTTATCCTAAAAATAGGGGGTTACAGTTGTGAATGTTTTA  
 TGTTTTGAATTTTGAATTTATTGTCTGATGAATAGTTGAGCTAAGCAAGCCCCGAATTTGATGATGTATAAAGT  
 GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT  
 CATTCCTATTGAGAACAGCTACCTTTGTGTAGGGAATAAGAGGTGACAGACAATAATGAACACACTCCCATATT  
 AACAGGACCTTTCTCAGTGAGCCATCTCACTCTGGAGAATGGTATGAATTTGGAGAGGTGCATTATTTCTTTC  
 TGGCCACTGGGGTTAAATTTAGTGTACTACAACATGATTTACTGAAGGCCACTAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGGAGTAAACAGTTTACAGAGAGAGTTTGGTGCTTAGTTATGTTGTTTTTAGATGATATACTAA  
 GCTCTACAGGGAAGAATGCTTAAATAATCTTTAATAAGATATGGGAAAAATTTTAAATAAACAGGAAACCA  
 TAATGATGTATATGCATCTGATGGGAAGGCATGAGATGGGATTTGTGAAGACAGAGGAAGACAGCCAT  
 AAATCTCTGGCTTTGGGGAACCTCATATCCCATGAAAAGGAAGAAACAATCAAAATAAGTGAGAGTAATGTAA  
 TGGAGCTCTTTCTCAGTAGGTTTATAGTAGCTGCCAATTTGTAATTCATCTGTTTAAAGAAAAATCTAGATTATTAAC  
 AACTGCTAGCAAAATCTGAGGAACATAAATTTCTCTGAAGAATCATAGGAAGATGACATTTTATTATAACC  
 ATATGATATCTCATATATATTTCTCTTTTAAAAAATATTTATCATCTCTGATATATTCTTTTATCTGCG  
 CTATTATCTCTCTGATATTGGAATTTGTGATTATATTGAGTGAATAGGAGAAAAATATATATACACACAGA  
 GAATTAAGAAAGTCACTTTCTGGGAGTGGGATATATTTGTTGAATACAGAACAGTGTAAATTTTAAAC  
 AACGGAAGGGTTAAATTAACCTCTTGACATCTTCATCTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAAT  
 GTAGTATTGTTTTGAATTTAAACAATAAAGCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFL  
 GSSEGLDFQTLLLEDERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD  
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNAGAKFIGTFF  
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRLINKWTTFLKARLIC  
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSVAVCVYSMADIRAVFNGP  
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
 AGGPTFKRINVDYRLTQIVVDHVIADGGQYDVMFLGTDIGTVLKVVISISKEKWNMEEVVLEE  
 LQIFKHSSIIINMELSLKQQQLYIGSRDGLVQLSLHRCDTYKGACADCCCLARDPYCAWDGNA  
 CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFFGIEFNSTFLECIPKSQQA  
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTNLN  
 VIENEQMENTQRAEHEEGQVKDLAESRLRYKDYIQLSSPNFSLDQYCEQMWHREKRQRN  
 KGGPKWKHMQEMKKRNRHHRDLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

10020063.121301

## FIGURE 177

CCCTGACCTCCCTGAGCCACTGAGCTGGAAGCCGAGAGGTCATCTCTGGAGCATGCCACC CGGGGAGCAGA  
 CAACCTCCCGAGTAGCTGGGAGCAAGAGCTGAAGCTGTTTCTCAGGAGCTGGGTGTTTTCCTCCACCCAC  
 CTCAGCAGTTTCAGCCAGCAGGGGACTGATCAGGTGTGTCTCTGGAGTGGGCGAGCAAGAGCGTGGCTGGCAGA  
 GTGGCTGGGAGAAAGAGGTTTCAGCGCTTGACCAAGCCGAGCTGCCCTGACTACAAGATCAGAAACCTGGGCATC  
 GGGTGAGGTGGGGGGGCGAGGTGTCATGTGACCTTCTGTCTCAGCAAGAGAGCTGAGAGAGGGGATCTTGG  
 AGCCATTGAGGGTGTGATGGAGCTACAGAGGGGAGGGAAAGGATATTTAAAGTTAAAGCTGTGGCACAATAGTTAA  
 GAGCAGAGTTTGGAGCTAGACCGACATAGGTTCAAATTTCTCTTGTGTTCTCTGTTGCTGTGAGCCCGAGT  
 AAGGGAGTGACTTAACCTCTCTGGAGTCAAATTTCTCATCACTAAAGTAGGGCCAATAATAGCAACCCACTCAT  
 AGGGAAGATTAAATGACATAATGTATGTGATGCAATGCAACTAGCAAAAGTACCAGTCCCATAGTAAGTCATGCCCACT  
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAAGGTAAGTCAACAGCTGGAGCAGAGGCGGCAGCAGGCT  
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGACAGGTGAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGCTGTCCAGAGGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTCGCC  
 CCCAAGCCCTGGCCACAGGGGCCCTCCCTGCCCTGCACACGTGGTATTTGCTATCAGGCAAGGGCTGAGGATG  
 AGCTGACAATCAGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC  
 AAGACGATGACATTCCTGCGGGGCGAGGCCACAGCATTCCTGGCCAGAGCCCTTACAGCTACACCCGAGAGA  
 GTGCAGAGAGCTGAGCTCCCTGAGGGGCACTCATCCGTGTGCTGCCCGGGCCCAAGATGAGATAGATGAGG  
 GCTTTCTGAGAGGGAGAATTTGGGGGGCGCTGTGGGGCTTCCCTCCCTGTGGTGGGAGAGCTGTCTGGCCGCC  
 CAGGCGCACTGAACTCTCTGACCTGAACAGATGCTCGCTGCCCTCTCTCCCTGAGCTTCTCCCACTGCAC  
 CTGACTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGCAAAAGCCCTGGACTTCCCTGGGTCTCTGG  
 ACATGATGAGCCACTCTCAGGCGGATGCGTCCACACCTTCCCGCGCGCTAAAGCCCGGATCTTGCCCAAC  
 CAGATCCCTCATCTGAGCTGAAGCCAGGGAAGCCTTGACCCCAAGTGATGCTGCTGTCCCTATCTCAAGCTTCGAGA  
 CCAACCATCAATGATCCAGAGCAACAGCCAAAGAGTGAATGCGCTTATTTCCACCTTCACTTCCAGGGT  
 GGAAGCTTGCCCTTCCCTATTTCTAGAGCTGGAACCCACTCCTTTTTCCTCAATGTCTATCATCTCTAGGACC  
 GGAATCACTACCTCTCTCTCTGATGACCTATAGGTTGGTGAATGCTGCTATCTCTGAGTCTCTAGGACC  
 ATCCATCAAGGTCTCTAGTGGATTATTGACAATGAATAAAGGGCACGAAGCCAGGCGAGGCTCGCAAGCAG  
 CCAGGGTCACTGGGGTGGGCTGGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGAGCGGATTATTGACAATGAATAAAGGGCACGAAGCCAGGCGAGGCGCTGGGCTCTTGTG  
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAAGGGGCCAACACGGGCGAGGGCTGCTCCAGCTTGCCAC  
 GCTCTATCATATGAGCGAGGTGTTGGGGAAGCGGGGCGAGGAGCTTTCAGCGCCACCCACCCCTGGCCCTGGTAG  
 TCCATCAGCACAATGAAGGAGACTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAGCTGTGTCCAGC  
 TTTTCCCTCGGGGCTCAGGACCTTCCCTACCTCCACCAACCAAGGAGGATTTATAGCAAGGCTAAGCCTGC  
 AGTTTACTCTGGGGGTTCAAGGAGCCGAAGGCTTAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACTCA  
 TTTAGGCTCAGGAGACTCACTCACATACCTCCTGCTCCTGTGGTAGAGACCTGAGAGAAAGGGGAGGGG  
 TCAACAATGAGAGACAGGAGTAGGTCTATCAGTGCCCCAGAGTAGAGAGCAATAGAGCCCGAGCCAGTGC  
 AGTCCCGCTGTGTTTCTTCACTGCTGGTGATCAGAAGTGTCTGGTTGGCTGCCATTGCTCTTGAAGTGG  
 CAGCCCTGGGCTTGGGCCCCCTCCCTCGGCCCCCTCAGTGTGGCTGTGCAGAGCTCTGGGGTTCCTTCAAGTG  
 GCAGGGGTGAGCTGCTGCTCCCTGAGTCCCTCATTTCTGACTGGGGGCTGGCTAGGACTGGGCTGTGGCC  
 TCTCAGGGGCGAGCTCTCATAGGCGAGGATCCTGCTTGGGCTGCCCTCCCGAGACCCCTGACCAACCCCTG  
 GGTCTGTCTCCCCAGGAGCCCGAGCTCCTGTCTGTGGGGAGCCATCAGGTGTCTGTGCAATGATGCGCT  
 TCTCAATGTGTGACCCGGAACCTGGGAGGGAGGGAACACTGGGTTTAGGACCACAACTCAGAGGCTGCTGT  
 GCCCTCCCTCTGAGCCAGGACATCTGAGTTTGGTGCTACTTCTCCCTGAGGACACTGCCAGGAGCCCTCTC  
 AGATTGTGGGGCACAATGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAGGCGCACTT  
 TTGGGATGAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACTGCCCACTGGCCCA  
 CAGAGAACAAGCTGGTCTCCCTGTCCGGGGCGGCTTTTCTTCTTGGAGCGTCCCTGACGGAACAAGTGGAG  
 GCTCTGCTGCGCTGCAATGCCAGTCAAGGGCTCAGAGGCTGCTGATGATGGGAGGGGCTC  
 CCGCTCTGAGGCTGGAGTGGCATCCACACTGGACAGCAGGAGGGGAGTGGGGTAACATTTTCATTTCCCT  
 TCACTGTTGTTTCTTCACTGTTCTTCACTGCTCTTAAACCCAGAGCCCAATTTCCCAAGCCCAATT  
 TTTCTGCTCTTATCTAATAAATCAATATTAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDAEIS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFQYQAGREDELTITTEGEWLEWIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSLPESQSDNPGCAEPTAFLAQALYSYTGQSAAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

10020053.121301



## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACCGAGAGACAGAGGAGGAAGAGACAGACAAAGCCACAGCGGAA  
 GAGGGCAGAGACAGGGCAGGCGACAGAGACAGAGCTCCTACAGAGGAGAGGCCACAGAGAGCTTGCAGA  
 AGACACAGCGAGGGAGAGACAAAGATCCAGGAAGAGGCGCTCAGCAGGACGATTTCGGAAGAGACAGCCCTGG  
 GCACCTCTCCCAAGCCCAAGGACTAGTTTTCTCCATTTCTCTTAAACGGTCTCCAGCCCTCTGAAGACTTTGCC  
 TCTGACCTTTGGCAGGATCCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGCAGGACTTCGT  
 GCCCTAGAGCGCCCTCAGTCCCTCCACGCTCGAGTACCAAGTGC~~ATG~~TCCAGACAGGCTCGCATCCCGGGAGGGG  
 CTTCGAGAGGGCGCTGGCTGTGGGAGGCCAACCCCTGCCCTCTGCTCCCCATTTGGCGGCTCTCTGGCTGGTGTG  
 GCTGCTTTCTGCTACTCTGCTGGCTCTCTCCCTGCCCTCAGCCCGGCTGGCCAGCCGCCCTCCCGGGAGGAGGAT  
 CGTGTTCAGAGAAAGCTCAACGCGAGCGTCTGCTGCTGGCTGGCGCCCTCGCAGGCTCTTTGGCGCTGTGA  
 GGCTTTGGGAGAGCGTCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCAGAGGGCTGACAGTGCAGTA  
 CCTGGGCGAGGCGCTGAGCTGCTGGGTGGAGCAGAGCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
 GGAGTCGGTGGCATCTCTGCACCTGGGATGGGGAGCCCTGTTAGCGCTGTGTACAATATCGGGGGGCTGAACTCCA  
 CCTCCAGCCCTGGAGGGAGGCCACCTTAACCTCTGCTGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC  
 TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGGCCAGCCCCAGCCAGCCGGAAGAGCCAA  
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCACCGTGC  
 GGGGCTTAAGCGCTACCTGCTAACAAGTGTGGCAGCAGCAGCCAAAGCCCTCAAGCACCCAAGCATCCGCAATCC  
 TGTCAAGCTTGGTGGTGACTCGGCTAGTGAATCTGGGGTCAGGCGAGGAGGGGCCCAAGTGGGGCCAGTGGCTGC  
 CCACAGCCCTGGCGAGCTTTCTGTGCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGGCCGTGACCACTTTGA  
 CACAGCCATTCCTGTATCCCGTCCAGGACTGTGTGGAGTCTCACTTCGCGACCTGGGTATGGCTGATGTGGG  
 CACCGTCTGTGACCCGGCTCGGAGTGTGCCATTTGTGGAGGATGAGGGCTCCAGTACGCTTCACTGTGCTCA  
 TGAACGGGTGCTGCTTCAACATGCTCCATGACAACCTCAAGCAGCTGATCAAGTTTGAATGGGCTTTGAGCAC  
 CTCTCGCCATGTCTATGCCGCCCTGTGATGGCTCATGTGGATCCTCGAGGAGGACCTGGTCCCCCTGCAAGTGGCCGT  
 CATCACTCTCTCTGACAGATGCTATGGGCACTGTCTCTTAGACAACACAGAGGCTCCATTCGACTCTGCTGT  
 GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGGCAGCTGACCTTCGGGCGGACTCAGCGCAATGTCC  
 AGACCTGGCCGCCGCCCTGTGCTGCCCTCTGCTGCTGGCCACCTCAATGGCCATCCGATGGCCAGTCCCAACAA  
 CTCGCCCTGGGCCGATGGCACCCCTCGGGGCCGACAGGCTGATGGTGTGCTGCTGCCCTCCACATGGACCA  
 GCTCCAGGACTTCAATATTCACACAGCTGGTGGCTGGGGCTCCTTGGGCGGCTGCTGCTGCCATGGACCA  
 TGGGGGTGGTGTCCAGTTCTCTCTCCGAGACTGCACAGGCGCTGTCCCCCGAATGTGTGCAAGTACTGTGAGGG  
 CGGCGGTACCGGCTTCGGCTCTGTCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCGCGAGGACCA  
 GTGTGCTGCTTCAACACCGCAGCCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGTCTCTCGCTACAC  
 AGCGGTGGCCCGCCAGGACAGTGCACAACTCACTGCCAGGCCCGGCGACTGGGCTACTAGTATGTGCTGGAGCC  
 ACGGGTGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCAGGGCCGATGCATCCATGCTGTGG  
 CTGTGATCGCATCATTTGGCTCCAAGAAAGTTTGAACAAGTGCATGGTGTGCGAGAGGAGCGGTCTGCTGTGAC  
 CAAGCAGTACGCTGCTTCAGGAAATTCAGGTACGGATACAACAATGTGTCAGCATATCCCCCGGCCCAACCCA  
 CATTTCTGTCCGGAGCAGGAGAAACCTTGGCCACCGGAGCATTACTTGGCCCTGAGGCTGCCAGTGTGCTCTTA  
 TGCCCTCAATGGCTTACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGGCAGTCACTCTTGGCCTA  
 CAGCGGGGCCACTCGACGCTCAGAGCACTGTCAAGGCACTGGGCCACTGGGCCAGCCCTTGACACTGCAAGTCTCT  
 AGTGGCTGGCAACCCAGGACACACGCTCCGATACAGCTTCTTCTGTCGGGCCGACCCCTTCAACGCCACG  
 CCCCACCTCCCAAGGACTGGCTGCACCAAGAGCAGATGTTGGAGATCCTTGGCGGGCGCCCTGGGCGGGCAG  
 GAAAT~~TAA~~CTCACTATCCGGCTGCCCTTCTGGGCAACGGGCTCCGAGCTTAAGTGTGGAGAAAGAGAGACTT  
 CTGTGCTGCTCATGCTCAAGACTAGTGGGGAGGGGCTGTGGGCTGTGAGACTGCCCTCTCTCTGCTCCATAT  
 GCGGAGGCTGCCCTGCCCTGGTTCTGCGCTTGGGAGCAGTGTGGTGTAGTGTGAGAGGGCTGACAGC  
 AGCCCTCCATCTAAACTGCCCTCTGCGCTGCGGGTACAGGAGGAGGGGGAAGCAGGAGGGGCTGGGCCCC  
 CAGTTGTATTTAGTATTTATTTACTTTATTTATTTAGCACAGGAGGGGCAAGGACTAGGCTGTGGGAA  
 CTGACCCCTGACCCCTCATAGCTCTACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTGT  
 TGTGTATGCGGTGCTGTGTGTGAAAATGTGTGTGTCTATGTATGATACAACTGTCTCTGCTCTCTCTCT  
 TTCTCGAATTTATTTTGGGAAAGAAAAGTCAAGGGTAGGGTGGGCTTCAGGAGATGAGGAGATATCTTTT  
 TTTTTTTCTTTCTTTCTTTCTTTTCTTTTTTTITGAGACAGAATCTGCTGTGCGCCAGGCTGGAGTGCATAG  
 GCACAACTCTGGCTCAGTCACTCTCCGCTTCCCGGCTTCAAGTATTCTCATGCCCTCAGGCTCTGTAGTGTG  
 GGATACAGGCTCTGCGCACCGCCAGCTAATTTTGTGTTTGTGTTGGAGAGGAGCTCTGCTATTTGTC  
 ACAGGCGCTGGAATGATTTCACTGCTGCAACCTTCGCCACCTGGGTTCCAGCAATTTCTCTGCTCAGCCCTCC  
 CGAGTAGCTGAGATATAGGCACCTACCAACACGCGCCAAATTTTGTATTTTGTAGTAGAGCGGGGTTTACAC  
 CATGTTGGCCAGGCTGGTCTGCAACTCTGACCTTAGGTGATCCACTGCGCTTATCATCCCAAGGTGCTGGGAT  
 ACAGGCGTAGAGCCAGCTGCTGGCCACGCGCAACTAATTTTGTATTTTGTAGTAGAGGTTTCCACTAT  
 TGGCCAGCTGCTCTTGAATCTCTGACCTCAGTAACTCGACTGCTCGGCTCCCAAGTGTGGGATACAGG  
 GTGAGGCCACCGCCGGTACATATTTTAAATTTGAATCTACTATTTATGTATCTTTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTCTCATTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTGAGGATTAATAATGTAATAAAGAACTACATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAGGAAA

10020068.121301

**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLPSARLASPLPREEEIV  
FPEKLNGLSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP  
ASGQGPCMNVKAPLGSPPSRPRRAKRFAASLSRFVETLVVADDKMAAFHAGLKRLLTVMAA  
AAKAFKHPSTIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSAIVEDDGLQSAFTAAHELGHVFNMLHD  
NSKPCISLNGPLSTSRHVMAVPMVAHVDPPEEPWSPCSARFITDFLNGYGHCLLDKPEAPLHL  
PVTFFPGKDYADARQCQLTFGPDSRHCPLPPCAALWC SGHLNGHAMCQTKHSPWADGTPCG  
PAQACMGGRCILHMDQLQDFNI PQAGGWGPWGPWGDCSRTC GGGVQVFSRDRCTRPVPRNGGKY  
CEGRRTFRSCNTEDCPTGSALT FREEQCAAYNHRTDLFKSFPGMDWVPRYTGVAPQDQCK  
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFKDKMVCVGGDG  
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLAKLPDGSYALNGEYTL  
MPSPTDVLVPGAVSLRYSGATAASETL SGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
PSTPRPTPDQDLHRRQAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT  
 AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAATTGATCCTGTG  
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
 TAAAAACGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
 TTAAAGTGATTCCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCC  
 GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAAAA

102063.12301

**FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTILVLFWGSKHFWEVPPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYGTIYFVLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEIEFDPMLDERGYCCIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCCAGGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
 GGCACCCTGCTTTGGCTGTCTGTCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC  
 CAGGGCCACCACGACCACTGCAAAACACGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCGGCGGGACTGTC  
 AATGGAGGCAGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

**FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLIITILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLIALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSIGGTLCLSCQ  
DEAPYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

10020053-121301

**FIGURE 185**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCTCGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
 GTCTGTGTTTGGCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCGAGCTGTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTG  
 GGCTGGGTCTGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTTCAGGCCAGCACTGGCTTTGGGTCCAACACCAAAACAAGAAG  
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTACCCAAAA  
 AACAAAGGAGATCCCATCTAGATTTCTTCTGTCTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCTCTAT  
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC  
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCAGCTTATCCCCAAGAAACTTTTGAAGGAAAGAGTAGACCCAAGATGTTATTTT  
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGGGCAACCAAACTTTCTACTG  
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
 TCCTCTTCTGTGCGGGGTGAGAAATTGTCCCTAGATGAATGAGAAAAATTATTTTTTTAAT  
 TTAAGTCTTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
 ATATAGCCTCACCCCTACATGTGGATAGAAGGAATGAAAAATAATTGCTTTGACATTGTCT  
 AATATGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAAGCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAAGCCAGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAA  
 ACTAATCTTTAA



**FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

10020063-121301

**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG  
 GAGTCCAGCTGGCTAAAACATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTC  
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCATAACTCAATAGTGAAT  
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT  
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTTACTATAAAGC  
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAAACTTTGATTTA  
 CTGTTCTTAACTGCTTAATCTTAATTACAGGAACGTGTGCATCAGCTATTTATGATTCTATAA  
 GCTATTTTACAGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAAATGACATTGCT  
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
 TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAACTCACTATTGCTTTTCAGGGAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAATGTTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA  
 AGATTAATAATGAAGGCTTAAATCAGCATTGTAAGGAAATGAATGGCTTTCTGATATGCTG  
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTCTCCCAGAGGCTTTTTTT  
 TTCTTGTTGATTAATAATTAACATTTTTAAACGCAGATATTTGTCAAGGGGCTTTCATTCA  
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
 GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTGGAAGAAGATGATGCATTTTGACAA  
 GAAATCATATATGATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
 AATAATAAATAAAGAGCAGAAAAATATGCTTGGTTTTTCATTTGCTTACCAAAAAACAACA  
 ACAAAAAAAGTTGCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG  
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA  
 ATCTGTAAATACTGTATTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA  
 AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTATA  
 TTAATAAATGTACATTTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSELLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

1020057.727301

**FIGURE 189**

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGACAGCACCAGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTGGCTGTGCTGCACTT  
GCCCCTCGGGGGGGTCCAGGGCCCCAGCCATTACATGGCCGCTACTCAACATCTGCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGCTCTGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCCTTTTGTCTGCTCCTGCTATTTTCTTTTACTGAGGATATTTAAATTCATTT  
GAAACTGAGCCAAGGTGTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCAAGAGTTCTCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGCTCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACTCTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

1020053.121301

**FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 23292, pI: 8.43, NX(S/T): 0  
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGLASLYLGWAASGLLLGGGLLCCTCP  
SGGSQGP SHYMARYSTSAPAIRGPEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

10020053.424304

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTATATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAATTCAGGAGTCCCTTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA  
ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
AGCGCTGCTGTCTCTTCTTATGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTTATAAAGTCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTACATTGATACGAAAGTTTCAATTGTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAGTATACCCATAATCATTAGCAAG  
TGTAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737  
><subunit 1 of 1, 173 aa, 1 stop  
><MW: 18938, pI: 9.99, NX(S/T): 1  
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRRKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

**Important features of the protein:****Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGATTAGTTTCTTTCACGATGGAAGTTGCTTAAATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTGAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

10020053.121301



**FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

10020063.121301

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGC GCCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCC**ATG**GCTGCCTCCCCGCGCGCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGTTAAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

1002063.121301

**FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNRNGHEYYGDYYQRHYD  
EDSAIGPRSPYGRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

10020053.121301

[illegible]

**FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPFPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRFFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

1022003.121301

**FIGURE 199**

GAGATTGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCTCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGGTCAGCAGC  
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCCTGGCTTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAATGCGGATGGAAGCTTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGAGGCATCCACTGCGCAAAAAGGA  
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAACAGGGTGCGGGTGACCGTGG  
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCCTCA  
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAAACCTGACCAGAGCCCCAGGAATAAA  
TGGTTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCCTGGTTCCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAGAAATCTTTATATTTATCG

10020053.121301

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNLLAGIHC AKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

10020063.121301

## FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCAGACACCTCATAGCAACCTATTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTCC  
 AATTTGAATCCCTGTGTAATGGGCTTTCAGAAGGCAATTAAGAATCACTCAGAGAGGAC  
 TTGGGGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGC  
 TGTTGGCAAATGTGAGGACAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGCATTG  
 CAGACTCCAGTTCTCTCTGCTGCTGCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGT  
 TGCACCTCCCCACCACACCTGACACGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGGTACAGCCCTCTGGAGGGCTGCCACCCTTTATCTCACTCGCGGAGGATCAGC  
 TGCTGGTGGCGTGGCTTACCCAGGCCAGAAGGAACCCAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCTCATCAAGCAGCCAAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGG  
 GGCTGATGAGGACGGGAGGTGTCTGAAGAAGAGGAGTTGACCCGTTGACCTGGACCCAC  
 GTGGCTCCAGGAGGCCTCAGTGCCCGCATCCCCCTCAGGAGGCTCTGCGGAGGTGCGG  
 CACCCACTGTGTCTGACAGCACCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
 TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCGACACAGTGC  
 CCAGGGCCTTCTGAAGGAGATCATCTCTGTGGACGACCTCAGCCAGCAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCAATGATGCCACTCCGAGTGCCACCCAGGCTGGCTGGAGCCCTCTCAGCAGAAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTAGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTCTGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGT  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT  
 TCCCCCTCGACAGGAGGCCACCCTGAGGAACAGGGTTCCGATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTACAAGCATAGCCAGAGGCCCTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTGTGCGGACATCCACTGG  
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCTGGGCT  
 GTCCCATTGGTGTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGACATTCATTTGGCAGCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAAGCAGCATGGGACTTCCAGG  
 AGAATGGGATGATGTGCCAATCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAGAAAAAC  
 AATAAAGATTGTACCTGCGTGGTGTGATGGAAGAACCCGCCAGCAGTGGCGATTGACCA  
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAAATTTTGGCCATC  
 AAAATCCAGTCCAAAGTGAACGTAAGAGCTTATATATTCTAGACTGATCCTTTGTGT  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTCATGTACTGCTGGCTGCTTA

1002063.121301



**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVS  
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSFVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVAILPCSRVGHYQNDQSHSPLDQEATL  
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLGCRTFHWFANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEGLAIHQHWFQENGMIHVHILSGKCMEAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

10020057.121301

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCTCCACACGCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACAGCCCCAGCC  
 CGCCCCCGCTGTGCCAGGGGAGGCCCTCGGCCACAGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCTGCTGGCACTG  
 CACCCCAAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTCAGCCCTCATGGCTCGCAACCCACACCCCACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTCGCGGCATTTC  
 CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCAAGCTCTATGTGACAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGAGCCAGAAAGC  
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCCACCCC  
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGGTGAGGGCGAGGGGCAATGGGATGGGAGGGCAAGGGAAGGGCAAC  
 TTAGGTCTTCAGAGCTGGGTGGGGTGGGCTGCGCTGAGTGGGTGAGGAGGAGCGGTGGC  
 CTTCCACAGCCCTGCGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCTTTC  
 CTCTCTCCAGTCTCTCAGGATCTGTGCTCTATTCTCTGCTGCCATAACTCCAACTCTGCCC  
 TCTTTGGTTTTTTTCTCATGCCACCTTGCTAAGACAACCTCGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGCTTTGAACCTCCCTTCTATCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCAATGTTGGGGTGACGCC  
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAGCCTTGACACACTCACCTCCACCTTAC  
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCCTTCCACATTTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTTCCCGGCTGATGTGTGGTGG  
 TGTGCGCGCTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCGCGAGCCCTCG  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCGTTGGGGCCTCATCGGTCATGG  
 TCTCGTCCCATTCACACCAATTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCCCAGACTCACCCCCAGCCCA  
 CTGCTAAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTGTCTTGTCTGTCCTGGCTG  
 TCTGTGTGTGGCCATCTCTGGACTTCAGAGCCCCGTGAGCCAGTCCCTCCCTTCCAGCCT  
 CCCTTTGGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCTTCCCTTCCCTTTGCTTCCCTGCCCTTCCCCCTCCTCAGGTT  
 CCTCCCTCCTTCCCTTCACTCTCCTTCCCTTTTGTCTTCCCTGCCCTTCCCCCTCCTCAGGTT  
 CTTCCTCCTTCTCAGTGGTTTTTCCACCTTCCCTTCCCTTCTTCCCTGGCTCCTTAGGCT  
 GTGATATATTTTTGTATTATCTCTTCTTCTTCTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAGCCTTTGCAAGATAA

10020063.121301

**FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASFPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV  
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEATIIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDAIWWGTCSDDYKPGDASTGWNSVSRITIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

10020063.121301

**FIGURE 205**

GTTAACAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCGGCGGGAGCCCGTGACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCTGCTGGGGCCCGGCCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCTGTCGCGCTGAGAAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGCGCGCGCGGCGCGACTCGGCAAAAAAAAAAAAAAAA

10620063.121301

**FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG  
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

4020053-121304

GGCGCTTGGTTGGTGCGCGCTGAAGGCTGTGGCGCGAGCAGCGCTGTTGGTTGGCCGCGGCG  
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGCGCTGGCCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATTGTGA  
ACTTCAAGTCTTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAG  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGAGGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCC  
CCAGAGGCGCTGGGAGTGTTCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGCAT  
CGACTGTCAAGCACCCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACACTGCACAG  
ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGAGGGGCTCCCCGCCTTCCAC  
CTGGCTGTATCGGGTAGGGCGGGGCGGTGGGTTACGGGCGCACCACTTACACAGCCTGTGT  
CCCACAGGTCCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCTGAATCCATTAATAAAC  
TGGCACAAGTAAGTCCGCTCCTCAAAACACACAGGCAGTGTGTATGTGAGCACTCGTG  
GGTAGTAGTGTGTGGGACAGGCTGGCTCCCTCAGCTCCCACTCTAGAGGGGCTCCCCGA  
GGAGGTGGAAGTGTGAAACCCAGCTCTGCGCAGGAGGCGCTGCAGTCTTTTCTCCCTCAAAG  
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCTCAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTTACAGACAGGACACGAGCATGAGGTAAGGCCG  
CCTGACCTGGACTTCAGGGGAGGGGGTAAAGGAGAGAGGAGGGGGCTAGGGGGTCTCTCT  
AGATCAGTGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCATGTGGTGGTTTCATGAACAGACCAGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGGCCACCCGGCCTTGTAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAAACACCGCTGCCGCGCCTGCACACCCCTTCGGACATCCCAGG  
ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCACCTGACCT  
TGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCTGCCCAACGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTGTGAGTGGGCTGCTGTGTG  
CTCAGGACCCCTCTCCGACCCGACAGCACTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAAGTCCGACAGCTGCGGGA  
TGTGATTAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLF

**Signal peptide:**

amino acids 1-15

10020053.121301

AGCAGGAGCAGGAGAGGGACA**AATG**GAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCT  
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCTG  
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC  
ACTGAGGTGGCTGTATAGGCTTCTTCCAGGATTAGAAATACCAGCAGTGCCCATACTCCA  
TAGCATGGTGCAAAAATTCACAGGCGTGTCATTTTGGGATCAGCACTGATTCTGAGGTTCTGA  
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCCGCTGGTAGACAAATGAACAACTG  
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
CAACAGCCTCCACATGGTGACAGAGTACAACCCCTGTGACTGTGATTGGGTTATTCAACAGCG  
TAATTCAGATTTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
CACAGATACCAGAAGGCACGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAACTAAGGAGTCTCACTGCCAG  
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
GTAGAGCATGTGCAAAATTTTGTGATGGATTCTAAGTGAAAAATTGTTGAAAGAAAATCG  
TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTCA**CTTCTCCTTGGAACACATATGGCC  
AAGTATCTACTTTATGCAAGGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
GATCACTAGGCCTGCCAACACACACACACGACGCACGTGCACACACGCACGCACGCTGCACAC  
ACACACGCGCACACACACACACACAGAGCTTCATTTCCCTGTCTTAAAATCTCGTTTTTCTC  
TTCTTCTCTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
CATACTCTGTAAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
CCTCTATGAAAGAGAGGCATTCTCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT  
TTGTATATCTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAAGTTACCTAAGGGT  
TGAAACTCTACCTTCTTTTATAAGCACATGTCCTGCTCTGACTCAGGATCAAAAACCAAAGG  
ATGGTTTTTAACACCTTTGTGAAATTGTCTTTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC  
CCTGAACCTCAGCAGAAATAGCCATTGTGAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCC  
TGTGTAATTAACAACCTGCATAATAATAATAAAGGCATCATGTTATA



**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRILDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVSHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

1000000.22301

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAAGCCTCTTCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGTCTGGCGGCGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCGAGTTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
 TGTCTGTAGAAAAGAGAATTTGCCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
 CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCAGATGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
 CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT  
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGA  
 TGAAGAGATGGTATGATTCTACATATGTACCATTTGTCTTGCTGTTTTTGTACTTTCTTTTC  
 AGGTCAATTTACAATTGGGAGATTTGAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAACTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
 AAATGTGCATATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG  
 GTCACCTTCACTCTGGACACAGTTGGATCAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTT  
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

10020053.121301

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510  
><subunit 1 of 1, 269 aa, 1 stop  
><MW: 29082, pI: 9.02, NX(S/T): 3  
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASININ  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI  
LAVLYRRKNKSKRDYTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

10020053.121301

**FIGURE 213**

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTGACAGTACTGCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGTCCATCAGCGCGCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCGCGGCCCCGACCTGAGGCG  
 TCGCCTCTGGCCGAGCGGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGCGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCCAGAGCCATCGAGAGAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC  
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
 CAGGGAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCACAGAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTTCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAGGCAAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTCAATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTGA  
 ACTTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTAAAAGTCAAATTTCTTTGTTTCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA  
 TGTTTATAAAGTAAAAAA

**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARATIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

10020063.123304

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTGCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAAG  
 GAATGGCTGTCCCACCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCAGATCGACACGCAAAAAAAAA

10020053.121701

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRI PRRPGALDGLEA  
GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETAFAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGSGLCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

1002005.12.30

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGAGCAGGTGCTCCGGGGGCCACC  
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAACTCTACCAGATTACTACTTCTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGT  
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGCCCTTCGAAACTGGGGGGAGAACTATGACC  
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCTGCCTGCCTCCTGTGCGACCGCCGC  
 GTGCTGTGCTGGGCACCATACAAGCTCTATTGAGAGTGTATCTTCATCTTTGTCTTCCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCCTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCCTAGGGCT  
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTGAGCATTGTGCTCTG  
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTGTAACCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATTGTACAGATCTCTCTGT  
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGTGATGGACTGGAAGAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTTAGAAA  
 ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

1020063.12301



**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQAFSRTCAGGLRCLLSDRR  
VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIISSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLI VVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
EQAGVLNWFVRPLHSLACLGLLVLDSDRKTGTRNMFICSAVMMALLAVVGLFTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

1002003.121301

**FIGURE 219**

GCGACGCGCGCGGGCGGGCGAGAGGAAACGCGGCGCGGGCGCGGGCCCGGCGCTGGAG**ATG**  
 GTCCCCGGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCTGGGGACATTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGTCTCGG  
 CCGAGACGGGTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGGT**TAGA**AGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCAAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT  
 CACCTGGCTCCAGCCTCCCTTACCCAGGGTCTCTGCACAGTGACCTTACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCCTCACTGACTTTTtagcaataaa  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

10020053.121301

**FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

10020063-121301

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTGCAGACTAGGTGGCAG  
AGGCCAACCCTAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAA**TAAA**AGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

1002005.121301

**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538  
><subunit 1 of 1, 116 aa, 1 stop  
><MW: 12910, pI: 6.41, NX(S/T): 1  
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW  
CCQTHDCCYDHLKTQCGGIYKDNKSSIHCMDLSQRYCLMAVFNVIIYLENEDSE

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCCAGGGGGCCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCAAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCAGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTGAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTACCCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTGCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAAGTGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

1002006-101201

**FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK  
LGDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

1002005-121301

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAAGTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTT  
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGGAGTGTCTGCGTGGCTGGCAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGTCCAAATTTTCTCTCTGGGTGTCAGCGAGCCCTGACTCAGTACAGTGCAGCTG  
 ACAGGGGCTGTGTCGCAACTGGCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATACAGAGATACCCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATCTTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAATTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCAGGAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGAACC  
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAATCTCACCTGGAGCAACAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAATCAGTGTATAG  
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
 GAAGCTTTTCAGTGGACCCAGTGTTCCTCAGTGTGTCCGAATCTGCAGCGCCTCAACCTTGA  
 TTCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGATTCTTGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAACTGGCTG  
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCGAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCGACGCGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCTGCCAGCATGAAGCAG  
 CTCGAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAAAT  
 GACTCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACGAGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCTTGCACCTATAACAAATCGGGCTCCAGGAGGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAGAGCTCTTAAAGCTGGGAAATTAAGTGGTGTCTTATTGAACCT  
 TGGTGACTATCAAGGGAACGCGATGCCCCCTCCCTCTCCCTCTCACTTTGGTGG  
 CAAGATCCTTCTTGTCCGTTTATGTGCATTATAATACTGGTCATTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGTTTAATATAA  
 TACCTATTGTATAAGACCTTTTACTGATTCCATTAATGTGCAATTTGTTTTAAGATAAACT  
 TCTTTCATAGGTAAAAA



amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
 TAAATATGTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
 TGTTTGGCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTGTGTGGAGACTTGGACTCTATTATGG  
 GACAGAAGCAGCTGTGAGTCCAACGTGTTGGAATTACCTTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCTTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATCCA  
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCAATA  
 GTCTGAGGAAGGACAATTCGACAAAAGAAATGGATGTTGGAAAAATTTTGGTCATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
 CTAGCATGGGGTCCATAAAAAATTATATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAGAACCGAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGGCCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
 AAACATCAATAGATATCTAAAAA

**FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

1002003.121301

**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCACTCCCACCCACCGGCGT  
 TTCTCCAGCTCCGATCTGGAGGCTGCTTCGCGAGTGTGGGACGCGAGCTGACGCCCGCTTATTA  
 GCTCTCGTGCCTCGCCCCGGCTCAGAAGCTCCGTGGCGCGGCGACCGTGACGAGAAGCCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAACT  
 CCCCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGATGGATACAACCTTGTCTGAAG  
 ATGAAGAATATACAAATATTGAGGATATTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGCTTCTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAAATATGTCCCAAAATTGAGTTTACTGTTCTTGTCTGATTGGACTCAT  
 TGGGGATTGATGTTTACTGCACCTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT  
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCTGGAAC  
 TCTAATTTCTGTACATAAAAAATTTTAAAGTTATTGTTTGTCTTTCAGGCAAGTCTGTTCAATG  
 CTGTAATATGTCCTTAAAGAGAATTTGGTAACCTGGTGTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCT  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTTGACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAATCATGACCCAAAGAAATGTATGATTGCACATCCTTCAGAAATAACTGA  
 AGGTTAATTATTGTATATTTTAAAAATTACCTTATAAGAGTATAATCTTGAATGGGTAG  
 CAGCCACTGTCATTAGCCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTCACATACATGAATGTTCATTTAAAGTTTAACTCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTCCATATTGGGGTAAATTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAA  
 GGTACTTTTTGTGTCGATTAATTAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCAATTTATATAATGGCCAC  
 GTAAAAATAAGAACATTTAAAAATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT  
 GTATATAGCACAGGGAACCCCTAATCTTGGGTAATTTCTAGTATAAACAATTTACTTTTTAT  
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
 CTCATATAGTAACGTATAAGTGACGTAGCTTCTAGATTTAGACTATATAGAAATTTAGATAT  
 TGTATTGTTGTCATTTAATATGTACCAACATGTAGCAATTAATCAATATTTATTAAAA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAATCTCTTCTCTTCTCTGTA  
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

**FIGURE 230**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
>>subunit 1 of 1, 140 aa, 1 stop
>>MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFLGIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLDDIILQLRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRNTNVSISR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAAACCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCTTGACTCGG  
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCCGTGCCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTACCAGCATCTCAACCACTGCC  
 TTCTCCCGCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCGACTTCGGG  
 AGGCTCAGTGCTGCCCTTACGACGCACAGTCAGGGCCGGGCACTACAGTGGACCTCTCC  
 CACAACCTCATTACCCGCTCGTGCCCAACCCACAGAGGGCCGGCTGCTGCGCCACCAT  
 TCAGAGCCTGAACCTGGCTGGAAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGGCC  
 TGCGCTACCTGAGCCTGGATGGAAACCTCTAGCTGTCTTGGTCCGGGTGCTTCGCGGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCTGCAGGTCTCTGGACCTGTCGGGCAACCCCAAGCTTAACT  
 GGGCAGGAGCTGAGGTGTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACTTGGTGCCCTGCCTGAGGCGCTGCTCTCCACCTCCCGGCACTGCAGAGCTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCTGGTGCGGGAGGGCACTACCCCGGAGGCTTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCAAC  
 ATCTTCT**TGA**CAAAATGGTGTGCCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCCTCAG  
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACAGTGGGGAGCCCGCAGGCCATATGTGGCA  
 GCGTCACCACAGAGGTTGTGGGCTTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCTCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCCTTCCCTCAT  
 GCCTGGGCGGCTGACCCGCAATGGGCAGAGGCTGGGTGGGACCCCTGCTCGAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGGCCATGGCCAGTCACTCAGGGGCGAGTT  
 TCTTTTCTAACTAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCTTCTCATGTGAC  
 AGATGGGAAACTGAGGCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCTTCTGCTCCAGCCCGGACCCAATGCACTTTCTGTCTCCTCTA  
 ATAAGCCCCACCTCCCGGCTGGGCTCCCTTGTGCTCCCTGGCTGTTCCTCCCATTAGCAC  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCAAAAGTGGGACTCTGGGCTCTGACAGCT  
 GTGGCGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
 CCAGCTTAGCCAGTTCTTACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAACCTTACC  
 CATTTTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGGCTTCTGGATTACGTCCTCCACTGGCCCTGAGCAGCAGCAG  
 CCTTCTTACCTTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
 TCTACCCCGAGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTCTTAGTCTTCATTTTA  
 TAAAGTTGTGCTTTTAAACGGAGTGTCACTTCAACCGGCTCCCTTACCCTGCTGGC  
 CGGGATGGAGCATGTCAATTGTAAAGCAGAAAAAGGTTGCATTGTTCACTTTTGTAAAT  
 ATTGTCTGGGCTGTGTTGGGTGTGGGGGAAGCTGGGCACTGGGCACTGGGCACTGGGCACT  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCTTAGC  
 CCATCATCTATCTAACCGGTCTTGATTAAATAAACATATAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

102003.121301

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652  
><subunit 1 of 1, 353 aa, 1 stop  
><MW: 37847, pI: 6.80, NX(S/T): 2  
MPWPLLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPT  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

1020063.127304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGTCT  
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAGATGGAACATTCACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
 GTACTAGTCTTGTGCTGGTACAGTGTATCTTATTTATGCATTACTTGTCTCCTTGCATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTGTGAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGTCTATTTAATGTATTT  
 ATTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAAAACCTTGTAATTCAGAAAGATGGCT  
 AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT  
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

1002006 121301  
 1002006 121301



**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGGATTGATNSHSDSELRP  
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKEANRCCLLRHLRLYLDRVFKNYQTP  
DHYTLRKISSLANSELTIKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALG  
ELDILLQWMEETE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAG  
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCTTATAGGGGAATGGTGCCGACA  
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
 TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG  
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
 GCTGGTGTTATTGGCCAGTTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTGAGATGCAAAT  
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTCTGGTGTACATCATGCATTG  
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAACACTACTTGGT  
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
 CGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT  
 TCAAGGTGAAGGATTATGAGTCTATATAAAGGCTTTTACCATCTGGCTGAGAATGACCC  
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
 TTTTAA

10020065-121301  
 10020065-121301

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH  
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRLKLEKPLRFRGVHHAFKILAEGLI  
RGLWAGWVPNIQRAALVNMGDLTTYDVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

10020063.721301

**FIGURE 237**

CGGACGCGTGGGCGGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCTCGCGCGCGC  
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAATTTATGCG  
 TTAAGAAGTAAAAATGCGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
 TCACACATGTGGTGTATTTTCCACATTGGCTTTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
 TTCATTGGTTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA  
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTTCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTGTTCCTTTACATTTTTATGTTC  
 TGAGTTTTGAAATAGTTTTATGAAATTCTTTATTTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCGTGAGATTTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCACTTTTAGAAGTAACCACTCTTGT  
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCGGG  
 CCGATTGCTTGAGGTCAAGTGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
 AAAAATACAAAAATAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
 TGCACCTCTAGCCTGGGGGAGAAAGTGAACCTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA  
 AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCG  
 AAAGGACTAGTTTGAAAGCTCTTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

**FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTEELWT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

10020053.121301

**FIGURE 239**

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGCCCGCAACACTCCGTCTCACCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCCAAGGTGTT  
 GGTCAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCCTTCACCTGGACAG  
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTGCTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATCCTTAAAGAAATCCGGGGGGTGCACTGGTGCTGGTGG  
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTGACTTG  
 GGGAGTTCCTACGCAAAACAACACTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAATAACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTAGGGTGCC  
 TGTGGCTCTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCC  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC  
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTCGTCAGGG  
 ACTGCTGACGGCTGGTCTGAGGAAGACAACTGCCAGACTTGAGCCCAATTAATTTTA  
 TTTTGTGCTGTTTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKYKCGLIKPCF  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

002063 12701

[illegible]



**FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812  
><subunit 1 of 1, 337 aa, 1 stop  
><MW: 37668, pI: 6.27, NX(S/T): 1  
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWHPASYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ  
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQLEKLQGTI  
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  
 GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGG  
 ATCAACTCGGTCAATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACGGCTC  
 CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG  
 ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG  
 AATGACACCTGGTACCAGACCCACCCATTGACCCTGGGAGGGTGAATGTACAACAGCAAC  
 TGCACCCACATGTGTTACCAATTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGC  
 TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCTTGTTCCTCCGGGAGGCAT  
 CCTGCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG  
 GAGCAGGTGTAATCCTGCCACCCAGGGAACCCAGCAGGCCGCTCCCAACTCCCAGTGGC  
 ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
 GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAGTGTTTCAAATTTTTCAACTAAG  
 CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA  
 GACACATTGGATAGTCTTAGAAGAAATTAATCTTTAATTTACCTGAAAATATCTTGAAATT  
 TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATCAATGGATAAAT  
 CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAACAATATTGGA  
 ACTGGA  
 AA  
 AAAAAAAAAAAAAAAAAAAAA

1020063.121304

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHHPVLPVFVTQLGAQGTLISSEE  
LPQIFTSLSLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLLTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

1020063.42301

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
 GAGCCAGACGCTGACCACGTTCTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG  
 GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCGCAGCGGCTCCGCGGCCTCC  
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
 GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG  
 GAGTCTGGACACCCAACCTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT  
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
 TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTGACGCTTGGTATTTACATTC  
 AATGGAGCTGAATGTTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG  
 CCCTGAAATGAATTCACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
 GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAA  
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**ATA**  
**AAT**GCCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCCTTGGAAATGGTTCACTTAAAT  
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTTACAGA  
 CCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCAATTTGCTTCAATCAAAGT  
 GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
 TAATTTGGAATATTGTTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
 TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
 AAAAAATTATTTCCAACA

1002006.121301

**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393  
><subunit 1 of 1, 243 aa, 1 stop  
><MW: 26266, pI: 8.43, NX(S/T): 1  
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV  
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

1002003.121201